

ALIGNMENTS

RESULT	1			
	RAY16727			
ID	AAY16727	standard;	Peptide;	156 AA.
XX				
AC	AAY16727;			
XX				
DT	17-AUG-1999	(first entry)		
XX				
DE	Human pre-pro persephin.			
KW	Growth factor; GF; persephin; neuron growth; cellular degeneration;			
KW	peripheral neuropathy; amytrophic lateral sclerosis; ischaemic stroke;			
KW	Alzheimer's disease; Huntington's disease; Huntington's disease; trauma;			
KW	brain injury; spinal cord injury; nervous system tumour; infection;			
KW	multiple sclerosis; cardiac muscle degeneration; injury; neurotoxin;			

and is derived by analysis of the total score distribution.

IMMUNOPOLY

Result No.	Query			DB ID
	Score	Match	Length	
1	839	100.0	156	20 AAY16727
2	839	100.0	156	21 AAY94038
3	554.5	66.1	183	22 AAB09563
4	554.5	66.1	183	23 ABG65476
5	530	63.2	156	20 AAY16724
6	529	63.1	96	20 AAY16731
7	513	61.1	141	22 ABC17121
8	511	60.9	156	20 AAY16721
9	504	60.0	91	20 AAY16732
10	492	58.6	89	20 AAY16733

W09914235-A1

1000

98WO-US19163 · 15-SEP-1998;

15 JUN 1977, 2703 0310-0.  
(UNIW ) UNIV WASHINGTON.  
Desauvage F., Johnson EM,  
Milbrandt JD;  
Lampe PA,  
Milbrandt JD;  
Klein R,  
Kotzbauer PT;  
McMurry, 1000 244022-00.



AC	AAB90563;	Oy	151 ACGCGG 156 
XX	01-JUN-2001 (first entry)	Db	178 LCGGG 183
DE	Human secreted protein, SEQ ID NO: 101.		
XX	Human; secreted protein; immunomodulatory; antisclerotic; dermatological; antiinflammatory; anti-HIV; cytosolic; cardiant; vascular; anti-angiogenic; ophthalmological; neuroprotectant; nociceptor; anticonvulsant; antialzheimer; anti-parkinsonian; antimicrobial; vunlear; vaccine; gene therapy; cancer; protein coordinate data; infection.		
XX	Homo sapiens.		
OS			
PN	WO200121658-A1.		
XX			
PD	29-MAR-2001.		
XX			
PT	22-SEP-2000; 2000WO-US26013.		
XX			
PR	24-SEP-1999; 99US-0155709.		
XX			
PA	(HUMA-) HUMAN GENOME SCI INC.		
XX			
PI	NI J, Baker KP, Birse CE, Ebner R, Fischella M, Komatsoulis GA; PI Lafleur DW, Moore PA, Olsen HS, Rosen CA, Ruben SA, Soppet DR; PI Young PE, Wei P, Florence KA;		
XX			
DR	WPI: 2001-235311/24.		
XX			
DR	N-PSDB; AAF57903.		
XX			
PT	Nucleic acids encoding 32 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. cancers, Parkinson's disease and diabetic retinopathy -		
PT			
XX			
PS	Claim 11; Page 787; 890pp; English.		
XX			
CC	The present sequence is one of 32 novel human secreted polypeptides. The nucleic acid molecules and polypeptides may be used in the prevention, diagnosis and treatment of diseases such as immune disorders (e.g. multiple sclerosis, systemic lupus erythematosus and human immunodeficiency virus (HIV) infections), hyperproliferative disorders (e.g. cancers and Gaucher's disease), cardiovascular diseases (e.g. Sickle cell syndrome, Chaga's cardiomyopathy and coronary artery occlousclerosis), angiogenic disorders (e.g. corneal graft neovascularisation and diabetic retinopathy), neurological disorders (e.g. Huntington's chorea, Alzheimer's disease and Parkinson's disease), infectious diseases and/or for promoting wound healing regeneration and/or chemotaxis. The nucleic acid molecules may be used to produce the secreted polypeptides. They may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acid sequences in samples. The polypeptides may be used as antigens in the production of antibodies and in assays to identify modulators of their expression and activity.		
XX			
SQ	Sequence 183 AA;		
	Score 66.1%; Score 554.5%; DB 22; Length 183;		
	Best Local Similarity 63.4%; Pred. NO. 4e-51; Gaps 5;		
	Matches 118; Conservative 5; Mismatches 30; Indels 33; Gaps 5;		
Qy	1 MAVGKFLLGSLLSLOLQGWGPARGYPVADGEFSSSEQVAKAGTTLWGLTH---RPLA 56	Oy	1 MAVGKFLLGSLLSLOLQGWGPARGYPVADGEFSSSEQVAKAGTTLWGLTDQFGSVTS 60
Db	1 MAVGKFLLGSLLSLOLQGWGPARGYPVADGEFSSSEQVAKAGTTLWGLTDQFGSVTS 60	Query Match 57 RPLA 56	Score 554.5%; DB 23; Length 183;
		Best Local Similarity 63.4%; Pred. NO. 4e-51;	
		Matches 118; Conservative 5; Mismatches 30; Indels 33; Gaps 5;	
Qy	1 MAVGKFLLGSLLSLOLQGWGPARGYPVADGEFSSSEQVAKAGTTLWGLTDQFGSVTS 60	Db	1 MAVGKFLLGSLLSLOLQGWGPARGYPVADGEFSSSEQVAKAGTTLWGLTDQFGSVTS 60
Qy	57 RPLA 56	Query Match 66.1%; Score 554.5%; DB 23; Length 183;	
Db	61 QSPALITLVTPALSPHRPPCPXPSPWPSPAVEPDPVRGPRGLRLIGE-VIF 90	Best Local Similarity 63.4%; Pred. NO. 4e-51;	
		Matches 118; Conservative 5; Mismatches 30; Indels 33; Gaps 5;	
Qy	91 RVAGSCPRGARTQHGLALARLOGOGRANGGCCPCCRPTRYTDVFLDDRHRWQLPOLSA 150	Oy	1 MAVGKFLLGSLLSLOLQGWGPARGYPVADGEFSSSEQVAKAGTTLWGLTDQFGSVTS 60
Db	119 RYAGSCPRGARTQHGLALARLOGOGRANGGCCPCCRPTRYTDVFLDDRHRWQLPOLSA 150	Query Match 61 RPLA 56	Score 554.5%; DB 23; Length 183;
		Best Local Similarity 63.4%; Pred. NO. 4e-51;	
		Matches 118; Conservative 5; Mismatches 30; Indels 33; Gaps 5;	



CC neurotoxins, metabolic diseases such as diabetes or renal dysfunctions  
 CC and damage caused by infectious agents. The GF can also be used for  
 CC promoting the growth and/or differentiation of a cell in a culture  
 CC medium. The antisense polynucleotides can be used for treating a disease  
 CC condition mediated by expression of persephin by a population of cells.  
 CC The products can also be used for detection and diagnosis.

XX Sequence 96 AA;

Query Match ABG17121  
 Best Local Similarity 100.0%; Pred. No. 9.4e-49;  
 Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 61 ALSPCPQLWSLTLISVAVELIGKTAEEKVPIRYCAGSCPRGARFQHGLALARLQGQRAHG 120  
 Db 1 ALSPCPQLWSLTLISVAVELIGKTAEEKVPIRYCAGSCPRGARFQHGLALARLQGQRAHG 60  
 Qy 121 GPCCRPTRTYDIAFLDDRRHQRLPOLSAAACGGC 156  
 Db 61 GPCCRPTRTYDIAFLDDRRHQRLPOLSAAACGGC 96

RESULT 7

ABG17121  
 ID ABG17121 standard; Protein; 141 AA.  
 AC ABG17121;  
 XX DT 18-FEB-2002 (first entry)  
 DE Novel human diagnostic protein #17112.

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
 food supplement; medical imaging; diagnostic; genetic disorder;  
 XX OS Homo sapiens.  
 XX PN WO200175067-A2.  
 XX PD 11-OCT-2001.  
 XX 30-MAR-2001; 2001WO-US08631.  
 XX 31-MAR-2000; 2000US-0540217.  
 PR 23-AUG-2000; 2000US-0649167.  
 XX PA (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;  
 XX PR; 2001-639362/73.  
 DR N-PSDB; AAS01308.

PT New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity -  
 XX PS Claim 20; SEQ ID NO 47480; 103pp; English.  
 XX The invention relates to isolated polynucleotide (I) and  
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
 CC and gene mapping, and in recombinant production of (II). The  
 CC polynucleotides are also used in diagnostics as expressed sequence tags  
 CC for identifying expressed genes. (I) is useful in gene therapy techniques  
 CC to restore normal activity of (II) or to treat disease states involving  
 CC (II). (II) is useful for generating antibodies against it, detecting or  
 CC quantitating a polypeptide in tissue, as molecular weight markers and as  
 CC a food supplement. (II) and its binding partners are useful in medical  
 CC imaging for sites expressing (II). (I) and (II) are useful for treating  
 CC disorders involving aberrant protein expression or biological activity.

CC The polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. ABG0010-ABG30377 represent novel human  
 CC diagnostic amino acid sequences of the invention.  
 CC Note: The sequence data for this patent did not appear in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.

CC diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. ABG0010-ABG30377 represent novel human  
 CC diagnostic amino acid sequences of the invention.  
 CC Note: The sequence data for this patent did not appear in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.

Sequence 96 AA;  
 SQ Score 529; DB 20; Length 96;  
 Best Local Similarity 100.0%; Pred. No. 9.4e-49;  
 Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 61 ALSPCPQLWSLTLISVAVELIGKTAEEKVPIRYCAGSCPRGARFQHGLALARLQGQRAHG 120  
 Db 1 ALSPCPQLWSLTLISVAVELIGKTAEEKVPIRYCAGSCPRGARFQHGLALARLQGQRAHG 60  
 Qy 121 GPCCRPTRTYDIAFLDDRRHQRLPOLSAAACGGC 156  
 Db 61 GPCCRPTRTYDIAFLDDRRHQRLPOLSAAACGGC 96  
 Sequence 141 AA;  
 SQ Score 513; DB 22; Length 141;  
 Best Local Similarity 98.0%; Pred. No. 7.7e-47;  
 Matches 97; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Qy 14 LSLOLGQWGDARGVVADEGFSSSEVAKAGGIVGTHPLAALRSGPQLWSLTL 73  
 Db 43 LGIHLGQGWGDARGVVADEGFSSSEVAKAGGIVGTHPLAALRSGPQLWSLTL 102  
 Qy 74 SVAELIGGYASEEKVIFRYCAGSCPRGARYQHGLALARL 112  
 Db 103 SVAELIGGYASEEKVIFRYCAGSCPRGARYQHGLALARL 141

RESULT 8

AAY16721  
 ID AAY16721 standard; Peptide; 156 AA.  
 XX DT 17-AUG-1999 (first entry)

Murine pre-pro persephin sequence.  
 DE DE Murine pre-pro persephin sequence.

XX Growth factor; GF; persephin; neuron growth; cellular degeneration;  
 KW peripheral neuropathy; amyotrophic lateral sclerosis; ischemic stroke;  
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease; trauma;  
 KW brain injury; spinal cord injury; nervous system tumour; infection;  
 KW multiple sclerosis; cardiac muscle degeneration; injury; neurotoxin;  
 KW metabolic disease; diabetes; renal dysfunction; neuritin.  
 XX Mus sp.  
 XX WO914235-A1.  
 XX PD 25-MAR-1999.  
 XX PP 15-SEP-1998; 98WO-US19163.  
 XX PR 16-SEP-1997; 97US-0931958.  
 XX PA (UNIW ) UNIV WASHINGTON.  
 XX Desauvage F, Johnson EM, Klein R, Kotzbauer PT;  
 PI Lampe PA, Milbrandt JD;  
 XX DR WPI; 1999-244023/20.  
 DR N-PSDB; AAX0489.

XX New isolated persephin growth factor nucleic acids used to, e.g.  
 PT promote neuronal growth  
 XX

Claim 5; Page 132; 222pp; English.

The invention relates to a novel isolated and purified growth factor (GF)  
 CC that comprises persephin or a fragment or a conservatively substituted  
 CC variant. The persephin GF polypeptides can promote the survival and  
 CC growth of neurons and non-neuronal cells. The persephin GF polypeptides  
 CC or polynucleotides can be used for preventing or treating cellular  
 CC degeneration or insufficiency, e.g. neuronal degeneration resulting from  
 CC peripheral neuropathy, amyotrophic lateral sclerosis, Alzheimer's  
 CC disease, Parkinson's disease, Huntington's disease, ischemic stroke,  
 CC acute brain injury, acute spinal cord injury, nervous system tumours,

CC multiple sclerosis, or infection, hematopoietic cell degeneration or insufficiency resulting from eosinopenia, anemias, thrombocytopenia, or stem-cell insufficiencies, cardiac muscle degeneration or insufficiency resulting from cardiomyopathy or congestive heart failure. They can also be used for treating e.g. peripheral nerve trauma or injury, exposure to neurotoxins, metabolic diseases such as diabetes or renal dysfunctions and damage caused by infectious agents. The GF can also be used for promoting the growth and/or differentiation of a cell in a culture medium. The antisense polynucleotides can be used for treating a disease condition mediated by expression of persephin by a population of cells. The products can also be used for detection and diagnosis.

XX Sequence 156 AA;

Query Match 60.9%; Score 511; DB 20; Length 156;

Best Local Similarity 64.2%; Pred. No. 1.4e-46; Matches 16; Gaps 3;

ID AAY16732 Standard; Peptide; 91 AA.

AC AAY16732;

DT 17-AUG-1999 (first entry)

DE WO9914235 Seq ID No: 221.

XX Growth factor: GF; persephin; neuron growth; cellular degeneration; peripheral neuropathy; amyotrophic lateral sclerosis; ischemic stroke; Alzheimer's disease; Huntington's disease; brain injury; spinal cord injury; nervous system tumour; infection; multiple sclerosis; cardiac muscle degeneration; injury; neurotoxin; metabolic disease; diabetes; renal dysfunction; neurturin.  
 XX Unidentified.  
 XX WO9914235-A1.  
 XX PD 25-MAR-1999.  
 XX PF 15-SEP-1998; 98WO-US19163.  
 XX PR 16-SEP-1997; 97US-0931858.  
 XX PA (UNIW ) UNIV WASHINGTON.  
 XX PT New isolated persephin growth factor nucleic acids used to, e.g. promote neuronal growth  
 XX PT Disclosure: Page 206-222pp; English.  
 XX PS CC The invention relates to a novel isolated and purified growth factor (GF) that comprises persephin or a fragment or a conservatively substituted variant. The persephin GF polypeptides can promote the survival and

CC growth of neurons and non-neuronal cells. The persephin GF polypeptides or polynucleotides can be used for preventing or treating cellular degeneration or insufficiency, e.g. neuronal degeneration resulting from peripheral neuropathy, amyotrophic lateral sclerosis, Alzheimer's disease, Parkinson's disease, Huntington's disease, ischemic stroke, acute brain injury, acute spinal cord injury, nervous system tumours, multiple sclerosis, or infection, hemopoietic cell degeneration or insufficiency resulting from eosinopenia, anemias, thrombocytopenia, or stem-cell insufficiencies, cardiac muscle degeneration or insufficiency resulting from cardiomyopathy or congestive heart failure. They can also be used for treating e.g. peripheral nerve trauma or injury, exposure to neurotoxins, metabolic diseases such as diabetes or renal dysfunctions and damage caused by infectious agents. The GF can also be used for promoting the growth and/or differentiation of a cell in a culture medium. The antisense polynucleotides can be used for treating a disease condition mediated by expression of persephin by a population of cells. The products can also be used for detection and diagnosis.

XX SQ Sequence 91 AA;  
 Query Match 60.1%; Score 504; DB 20; Length 91;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-6; Mismatches 0; Indels 0; Gaps 0;  
 Matches 91; Conservative 0; Peptide: 89 AA.  
 YY QY 1 MAVGKFLLSLLSLQLGQWGPARGVPADEFSSEQVAKAGGTWL---GTHRPLR 57  
 YY QY 1 MAGRLRLCLLCLSLHPSLGWLDLQEASAVD-KLSFGKMAETRGTWTPHGNHH-VR 57  
 YY 58 LRALSLCPLWLSLTLVSEKVKIYRCAGSCPGRGARTQHGLALARLQGGR 117  
 YY 58 LRALAGSCRWLWLSLTLVPAELGIGYASEEKVKIYRCAGSCPGRGARTQHSLVLRGR 117  
 DB 118 AHGGPCRPRPTYTDVAFDRHRWQLRPOSAACCGG 156  
 QY 118 AHGRPCCQPTSYADTFDQHWMQQLPOLSAACCGG 156  
 DB 118 AHGRPCCQPTSYADTFDQHWMQQLPOLSAACCGG 156  
 YY QY 126 PTRYTDAFLEDRHRWQLPQLSAAACCGG 156  
 DB 61 PTRYTDAFLEDRHRWQLPQLSAAACCGG 91

RESULT 9  
AAY16732

ID AAY16733 standard; Peptide: 89 AA.  
 AC AAY16733;  
 DT 17-AUG-1999 (first entry)  
 DE Human persephin protein.  
 XX DE Human persephin protein.  
 XX KW Growth factor; GF; persephin; neuron growth; cellular degeneration; peripheral neuropathy; amyotrophic lateral sclerosis; ischemic stroke; Alzheimer's disease; Huntington's disease; brain injury; spinal cord injury; nervous system tumour; infection; multiple sclerosis; cardiac muscle degeneration; injury; neurotoxin; metabolic disease; diabetes; renal dysfunction; neurturin.  
 XX KW Homo sapiens.  
 OS XX PN WO9914235-A1.  
 OS XX PD 25-MAR-1999.  
 OS XX PF 15-SEP-1998; 98WO-US19163.  
 OS XX PR 16-SEP-1997; 97US-0931858.  
 OS XX PA (UNIW ) UNIV WASHINGTON.  
 OS XX DR WO1999-244023/20.  
 OS XX PT New isolated persephin growth factor nucleic acids used to, e.g. promote neuronal growth  
 OS XX PT Disclosure: Page 206-222pp; English.  
 OS XX PS CC The invention relates to a novel isolated and purified growth factor (GF) that comprises persephin or a fragment or a conservatively substituted variant. The persephin GF polypeptides can promote the survival and

CC growth factor nucleic acids used to, e.g. promote neuronal growth  
 CC XX PT PS CC The invention relates to a novel isolated and purified growth factor (GF) that comprises persephin or a fragment or a conservatively substituted variant. The persephin GF polypeptides can promote the survival and



CC Huntington's disease, diabetes, acquired immunodeficiency syndrome  
 CC (AIDS), ischaemic stroke, acute brain injury, acute spinal cord injury,  
 CC multiple sclerosis, nervous system tumours (e.g. neuroblastomas), or  
 CC enteric diseases such as idiopathic constipation. The sequences are also  
 CC useful for preventing or treating cellular degeneration or insufficiency  
 CC in an individual, suffering from eosinopaenia, basopaenia, lymphopaenia,  
 CC monocytopenia, neutropaenia, anaemia, thrombocytopaenia, cardiac muscle  
 CC degeneration, or congestive heart failure. The growth factors are also  
 CC useful for promoting the survival of peripheral and central neuronal  
 CC populations *in vivo* or *in vitro*.

XX Sequence 89 AA:

Query Match	58.5%	Score 492;	DB 22;	Length 89;
Best Local Similarity	100.0%	Pred. No.	7	6e-45;
Matches	89;	Mismatches	0;	Indels 0;
Gaps	0;			

Qy 66 CQWLSLTSLVAELGLGYYASEKVIFRYCAAGSCPRGARTQHGLALARLOGOGRAHGSPCCR 125  
 1 CQWLSLTSLVAELGLGYYASEKVIFRYCAAGSCPRGARTQHGLALARLOGOGRAHGSPCCR 60

Db 126 PTRYTDVAFLDDRHMRQLDRLWQLPQLSAAACGGC 154  
 61 PTRYTDVAFLDDRHMRQLDRLWQLPQLSAAACGGC 89

PS Claim 8; Page 48; 73pp; English.

XX The sequence represents a human persephin full-length protein, whereby  
 CC the F2a and F2c regions have amino acid substitutions from the F2a and  
 CC F2c regions of artemin protein. Persephin can have substitutions from  
 CC the F2a and F2c regions of the proteins GDNF, neururin and artemin, from  
 CC humans, mice or rats. This type of protein activates the growth factor  
 CC receptor alpha1-Ret protein-tyrosine kinase (GFRalpha1-RET), but does not  
 CC substantially activate GFRalpha2-RET or GFRalpha3-RET. The growth factors  
 CC and nucleic acids encoding them are useful for providing trophic support  
 CC to a mammalian cell and/or for producing differentiation of a mammalian  
 CC cell, in a patient suffering from peripheral neuropathy, amyotrophic  
 CC lateral sclerosis, Alzheimer's disease, Parkinson's disease, Huntington's  
 CC disease, diabetes, acquired immunodeficiency syndrome (AIDS), ischaemic  
 CC stroke, acute brain injury, acute spinal cord injury, multiple sclerosis such as  
 CC nervous system tumours (e.g. neuroblastomas), or enteric diseases such as  
 CC idiopathic constipation. The sequences are also useful for preventing or  
 CC treating cellular degeneration or insufficiency in an individual,  
 CC suffering from eosinopaenia, basopaenia, lymphopaenia, neutropaenia,  
 CC anaemia, thrombocytopaenia, cardiac muscle degeneration, or  
 CC congestive heart failure. The growth factors are also useful for  
 CC promoting the survival of peripheral and central neuronal populations *in*  
 CC *vivo* or *in vitro*.

SQ Sequence 96 AA:

Query Match 58.4%; Score 490; DB 22; Length 96;  
 Best Local Similarity 92.7%; Pred. No. 1 4e-44;  
 Matches 89; Conservative 3; Mismatches 4; Indels 0;  
 Gaps 0;

Qy 61 ALSGPCOLWSLTSLVAELGLGYYASEKVIFRYCAAGSCPRGARTQHGLALARLOGOGRAHG 120  
 1 ALSGPCOLWSLTSLVAELGLGYYASEKVIFRYCAAGSCPRGARTQHGLALARLOGOGRAHG 60

Db 121 GPCCRPTRYTDVAFLDDRHMRQLDRLWQLPQLSAAACGGG 156  
 61 GPCCRPTRYTDVAFLDDRHMRQLDRLWQLPQLSAAACGGG 96

RESULT 14

AAU03950 standard; Protein: 97 AA.

AAU03950;

AAU03950; 23-OCT-2001 (first entry)

DE Human PAP-F2ac full-length polypeptide.  
 XX Persephin; F2a; F2c; GDNF; neururin; artemin; human; mouse; rat; AIDS;  
 KW growth factor receptor alpha1-Ret protein tyrosine kinase; GFRalpha1-RET;  
 KW trophic support; peripheral neuropathy; amyotrophic lateral sclerosis;  
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease; diabetes;  
 KW acquired immunodeficiency syndrome; ischaemic stroke; acute brain injury;  
 KW acute spinal cord injury; multiple sclerosis; nervous system tumour;  
 KW neuroblastoma; enteric disease; idiopathic constipation; eosinopaenia;  
 KW basopaenia; lymphopaenia; monocytopaenia; neutropaenia; anaemia;  
 KW cardiac muscle degeneration; congestive heart failure; thrombocytopaenia;  
 KW mutant; mutein.

OS Chimeric - Homo sapiens.

XX Key Location/Qualifiers

FT Region 68..72 "Human artemin F2a region"  
 FT Region 82..88 "Human artemin F2c region"

XX WO200147946-A2.

PD 05-JUL-2001.

PP 21-DEC-2000; 2000WO-US34852.

PR 28-DEC-1999; 99US-0473551.

PA (UNIV ) UNIV WASHINGTON.

PI Milbradt JD, Baloh RH;

DR 2001-425618/45.

XX WO200147946-A2.

XX PN 05-JUL-2001.

XX PD 21-DEC-2000; 2000WO-US34852.

PP

XX Key Location/Qualifiers  
 FT Region 68..72 "Human neururin F2a region"  
 FT Region 82..88 "Human neururin F2c region".

XX WO200147946-A2.

XX PN 05-JUL-2001.

XX PD 21-DEC-2000; 2000WO-US34852.

PP



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Om<sub>n</sub> protein - protein search, using sw model

Run on: July 11, 2003, 12:46:08 : Search time 14 Seconds  
(without alignments)

327.855 Million cell updates/sec

Title: US-09-220-617B-217

Perfect score: 839

Sequence: 1 MAYGKFLIGSLLSSLQGQ.....DRHRWQWLRLQLSAAACCGG 156

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seeds, 2942922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%  
Listing first 45 summaries

## Database :

- Issued\_Patents\_AA:\*
  - 1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.PEP:\*
  - 2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.PEP:\*
  - 3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.PEP:\*
  - 4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.PEP:\*
  - 5: /cgn2\_6/ptodata/1/1aa/PCMS\_COMB.PEP:\*
  - 6: /cgn2\_6/ptodata/1/1aa/backfiles.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	839	100.0	156	4	US-09-931-8585-217	Sequence 217, APP
2	724	86.3	133	4	US-09-931-8585-192	Sequence 132, APP
3	530	63.2	156	4	US-09-931-8585-196	Sequence 196, APP
4	529	63.1	96	4	US-09-931-8585-221	Sequence 221, APP
5	529	63.1	96	4	US-09-220-528-15	Sequence 15, APP
6	511	60.9	156	4	US-09-931-8585-185	Sequence 185, APP
7	492	58.6	89	4	US-09-931-8585-223	Sequence 223, APP
8	492	58.6	89	4	US-09-931-8585-18	Sequence 18, APP
9	452	53.9	185	4	US-09-981-739-133	Sequence 133, APP
10	452	53.9	185	4	US-09-128-026-133	Sequence 133, APP
11	451	53.8	134	4	US-09-981-739-81	Sequence 1, APP
12	451	53.8	134	4	US-09-128-026-81	Sequence 81, APP
13	451	53.8	142	4	US-09-931-8585-111	Sequence 111, APP
14	451	53.8	142	4	US-09-128-016-111	Sequence 111, APP
15	53.8	142	4	US-09-128-016-111	Sequence 111, APP	
16	447	53.3	185	4	US-09-981-739-136	Sequence 136, APP
17	447	53.3	185	4	US-09-128-026-136	Sequence 136, APP
18	439	52.3	96	4	US-09-931-8585-80	Sequence 10, APP
19	439	52.3	96	4	US-09-931-8585-187	Sequence 187, APP
20	439	52.3	96	4	US-09-981-739-80	Sequence 80, APP
21	439	52.3	96	4	US-09-128-026-80	Sequence 80, APP
22	433	51.6	96	4	US-09-931-8585-198	Sequence 198, APP
23	425	50.7	91	4	US-09-931-8585-89	Sequence 89, APP
24	425	50.7	91	4	US-09-981-739-89	Sequence 89, APP
25	425	50.7	91	4	US-09-128-026-89	Sequence 89, APP
26	423	50.4	91	4	US-09-931-8585-83	Sequence 83, APP
27	423	50.4	91	4	US-09-981-739-83	Sequence 83, APP

## ALIGNMENTS

RESULT 1	US-09-931-8585-217	Sequence 217, Application US/08931858E
; GENERAL INFORMATION:	; ;	; ;
; APPLICANT: JOHNSON, EUGENE M	; ;	; ;
; ; MILLERDIT, JEFFREY D	; ;	; ;
; ; KOTZBAUER, PAUL T	; ;	; ;
; ; LAMPE, PATRICIA A	; ;	; ;
; ; KLEIN, ROBERT	; ;	; ;
; ; DESAUVAGE, FRED	; ;	; ;
; TITLE OF INVENTION: PESEPHIN AND RELATED GROWTH FACTOR	; ;	; ;
; NUMBER OF SEQUENCES: 239	; ;	; ;
; CORRESPONDENCE ADDRESS:	; ;	; ;
; ADDRESS: HOWELL & HAERKAMP, L.C.	; ;	; ;
; STREET: 7733 FORSYTH BOULEVARD, SUITE 1400	; ;	; ;
; CITY: ST. LOUIS	; ;	; ;
; STATE: MO	; ;	; ;
; COUNTRY: USA	; ;	; ;
; ZIP: 63105	; ;	; ;
; COMPUTER READABLE FORM:	; ;	; ;
; MEDIUM TYPE: Floppy disk	; ;	; ;
; COMPUTER: IBM PC compatible	; ;	; ;
; OPERATING SYSTEM: PC-DOS/MS-DOS	; ;	; ;
; SOFTWARE: Patent Release #1.0, Version #1.30	; ;	; ;
; CURRENT APPLICATION DATA:	; ;	; ;
; APPLICATION NUMBER: US/08/931,858E	; ;	; ;
; FILING DATE:	; ;	; ;
; CLASSIFICATION: 435	; ;	; ;
; ATTORNEY/AGENT INFORMATION:	; ;	; ;
; NAME: HOLLAND, DONALD R.	; ;	; ;
; REGISTRATION NUMBER: 35,197	; ;	; ;
; REFERENCE/DOCKET NUMBER: 971486	; ;	; ;
; TELECOMMUNICATION INFORMATION:	; ;	; ;
; TELEPHONE: 314-727-5188	; ;	; ;
; TELEFAX: 314-727-6092	; ;	; ;
; INFORMATION FOR SEQ ID NO: 217:	; ;	; ;
; SEQUENCE CHARACTERISTICS:	; ;	; ;
; LENGTH: 156 amino acids	; ;	; ;
; TYPE: amino acid	; ;	; ;
; STRANDEDNESS:	; ;	; ;
; TOPOLOGY: linear	; ;	; ;
; MOLECULAR TYPE: peptide	; ;	; ;
; US-08-931-8585-217	; ;	; ;
Query Match Score 839; DB 4; Length 156;		
Best Local Similarity 100.0%; Pred. No. 4e-88;		
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		

Qy

1 MAVGFLGLSSLLSLLQLGGWGPDARGVPVADGEFSSEQQVAKAGGTWLGTPLRLRR 60

Db 1 MAYGRFLGSSLILSLQLQGKRPDARGPVADGEFSEQQAKAGTTLGTHPLRLRR 60  
 Qy 61 ALSGPCQLNSLTLISVAEGLGTAASSEEKVTFRICAAGSCPRGARTQGLALRLOGQRAHG 120  
 Db 61 ALSGPCQLNSLTLISVAEGLGTAASSEEKVTFRICAAGSCPRGARTQGLALRLOGQRAHG 120  
 Qy 121 GPCCRPRTYTDVAFELDDHRWLPOLSAAAACGGG 155  
 Db 121 GPCCRPRTYTDVAFELDDHRWLPOLSAAAACGGG 155

**RESULT 2**  
 US-08-931-858E-132  
 Sequence 1.32, Application US/08931858E  
 GENERAL INFORMATION:  
 Patent No. 6222022  
 COMPUTER READABLE FORM:  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 NUMBER OF SEQUENCES: 239  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: HOWELL & HAERKAMP, L.C.  
 STREET: 7733 FORSYTH BOULEVARD, SUITE 1400  
 CITY: ST. LOUIS  
 STATE: MO  
 ZIP: 63105  
 COMPUTER READABLE FORM:  
 COMPUTER: IBM PC compatible  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/931,858E  
 FILING DATE:  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: HOLLAND, DONALD R.  
 REGISTRATION NUMBER: 971486  
 REFERENCE/DOCKET NUMBER: 971486  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 314-727-5188  
 TELEX/FAX: 314-727-6032  
 INFORMATION FOR SEQ ID NO: 196:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 156 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: Linear  
 MOLECULE TYPE: peptide  
 US-08-931-858E-196

Query Match 63.2%; Score 530; DB 4; Length 156;  
 Best Local Similarity 66.0%; Pred. No. 6.9e-33; Mismatches 35; Indels 6; Gaps 3;  
 Matches 105; Conservative 13; Query Match 63.2%; Score 530; DB 4; Length 156;  
 Qy 1 MAVGKFLIGSLLLSLQLGQNGPDARGPVADGEFSEQQAKAGTTLGTHPLRLRR 57  
 Db 1 MAAGRRLRFLFLSLSLAUGLGWLQLEAPAD-ELSGRMATECRTWKPHQGNNN-VR 57  
 Qy 58 IARRALSGPCQLNSLTLISVAEGLGTAASSEEKVTFRICAAGSCPRGARTQGLALRLOGQGR 117  
 Db 58 IPRALPGCLRWLSLTPAELGLGTAASSEEKVTFRICAAGSCPRGARTQGLALRLOGQGR 117  
 Qy 118 AHGGPCCRPRTYTDVAFELDDHRWLPOLSAAAACGGG 156  
 Db 118 AHGRPCQCQPTSYADYTFLDDHHWQQLPOLSAAACCGG 156  
**RESULT 4**  
 US-08-931-858E-221  
 Sequence 221, Application US/08931858E  
 GENERAL INFORMATION:  
 Patent No. 6222022  
 COMPUTER READABLE FORM:  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 NUMBER OF SEQUENCES: 239  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: HOWELL & HAERKAMP, L.C.  
 STREET: 7733 FORSYTH BOULEVARD, SUITE 1400  
 CITY: ST. LOUIS  
 STATE: MO  
 ZIP: 63105  
 COMPUTER READABLE FORM:  
 COMPUTER: IBM PC compatible  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/931,858E  
 FILING DATE:  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: HOLLAND, DONALD R.  
 REGISTRATION NUMBER: 971486  
 REFERENCE/DOCKET NUMBER: 971486  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 314-727-5188  
 TELEX/FAX: 314-727-6032  
 INFORMATION FOR SEQ ID NO: 132:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 133 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: Linear  
 MOLECULE TYPE: peptide  
 US-08-931-858E-132

Query Match 86.3%; Score 724; DB 4; Length 133;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-15; Mismatches 0; Indels 0; Gaps 0;  
 Matches 133; Conservative 0; Query Match 86.3%; Score 724; DB 4; Length 133;  
 Qy 1 PDARGPVADGEFSEQQAKAGTTLGTHPLRLRR 83  
 Db 1 PDARGPVADGEFSEQQAKAGTTLGTHPLRLRR 83  
 Qy 84 SEEKVTFRICAAGSCPRGARTQGLALRLOGQRAHGPGCCRTRYTDVAFELDDHRWQR 143  
 Db 61 SEEKVTFRICAAGSCPRGARTQGLALRLOGQRAHGPGCCRTRYTDVAFELDDHRWQR 120  
 Qy 144 LPQLSAAACGGG 156  
 Db 121 LPQLSAAACGGG 133

APPLICANT: DESAUVAGE, FRED  
TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTOR  
NUMBER OF SEQUENCES: 239  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HOWELL & HAERKAMP, L.C.  
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400  
CITY: ST. LOUIS  
STATE: MO  
ZIP: 63105  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS DOS  
SOFTWARE: Patentin Release #1.0, version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/931,858E  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: HOLLAND, DONALD R.  
REGISTRATION NUMBER: 35,197  
REFERENCE/DOCKET NUMBER: 971486  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 314-727-5188  
TELEFAX: 314-727-5092  
INFORMATION FOR SEQ ID NO: 221:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 96 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-931-858E-221

Query Match 63.1%; Score 529; DB 4; Length 96;  
Best Local Similarity 100.0%; Pred. No. 4.8e-53;  
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Patent No. 6222022  
GENERAL INFORMATION:  
APPLICANT: JOHNSON, EUGENE M  
APPLICANT: MILBRANDT, JEFFREY D  
APPLICANT: KOTZBAUER, PAUL T  
APPLICANT: LAMPE, PATRICIA A  
APPLICANT: KLEIN, ROBERT  
APPLICANT: DESAUVAGE, FRED  
TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTOR  
NUMBER OF SEQUENCES: 239  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HOWELL & HAERKAMP, L.C.  
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400  
CITY: ST. LOUIS  
STATE: MO  
COUNTRY: USA  
ZIP: 63105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/931,858E  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: HOLLAND, DONALD R.  
REGISTRATION NUMBER: 35,197  
REFERENCE/DOCKET NUMBER: 971486  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 314-727-5188  
TELEFAX: 314-727-6092  
INFORMATION FOR SEQ ID NO: 185:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 156 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-931-858E-185

Query Match 60.9%; Score 511; DB 4; Length 156;  
Best Local Similarity 64.2%; Pred. No. 1e-50;  
Matches 102; Conservative 16; Mismatches 35; Indels 6; Gaps 3;  
Patent No. 6284540  
GENERAL INFORMATION:  
APPLICANT: Milbrandt, Jeffrey D.  
APPLICANT: Baloh, Robert H.  
TITLE OF INVENTION: Artemin, A No. 6284540el Neurotrophic Factor  
FILE REFERENCE: 6029-7998  
CURRENT APPLICATION NUMBER: US/09/220,528A  
CURRENT FILING DATE: 1998-12-24  
EARLIER APPLICATION NUMBER: 09/218,698  
EARLIER FILING DATE: 1998-12-22  
EARLIER APPLICATION NUMBER: 60/108,148  
EARLIER FILING DATE: 1998-11-12  
EARLIER APPLICATION NUMBER: 09/163,283  
EARLIER FILING DATE: 1998-09-29  
NUMBER OF SEQ ID NOS: 120  
SEQ ID NO 15  
LENGTH: 96  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-220-528-15

Query Match 63.1%; Score 529; DB 4; Length 96;  
Best Local Similarity 100.0%; Pred. No. 4.8e-53;  
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Patent No. 6222022  
GENERAL INFORMATION:  
APPLICANT: JOHNSON, EUGENE M  
APPLICANT: MILBRANDT, JEFFREY D  
APPLICANT: KOTZBAUER, PAUL T  
APPLICANT: LAMPE, PATRICIA A  
APPLICANT: KLEIN, ROBERT  
APPLICANT: DESAUVAGE, FRED  
TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTOR  
NUMBER OF SEQUENCES: 239  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HOWELL & HAERKAMP, L.C.  
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400  
CITY: ST. LOUIS  
STATE: MO  
COUNTRY: USA  
ZIP: 63105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/931,858E  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: HOLLAND, DONALD R.  
REGISTRATION NUMBER: 35,197  
REFERENCE/DOCKET NUMBER: 971486  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 314-727-5188  
TELEFAX: 314-727-6092  
INFORMATION FOR SEQ ID NO: 185:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 156 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-931-858E-185

Query Match 58.9%; Score 511; DB 4; Length 156;  
Best Local Similarity 64.2%; Pred. No. 1e-50;  
Matches 102; Conservative 16; Mismatches 35; Indels 6; Gaps 3;  
Patent No. 6284540  
GENERAL INFORMATION:  
APPLICANT: Milbrandt, Jeffrey D.  
APPLICANT: Baloh, Robert H.  
TITLE OF INVENTION: Artemin, A No. 6284540el Neurotrophic Factor  
FILE REFERENCE: 6029-7998  
CURRENT APPLICATION NUMBER: US/09/220,528A  
CURRENT FILING DATE: 1998-12-24  
EARLIER APPLICATION NUMBER: 09/218,698  
EARLIER FILING DATE: 1998-12-22  
EARLIER APPLICATION NUMBER: 60/108,148  
EARLIER FILING DATE: 1998-11-12  
EARLIER APPLICATION NUMBER: 09/163,283  
EARLIER FILING DATE: 1998-09-29  
NUMBER OF SEQ ID NOS: 120  
SEQ ID NO 15  
LENGTH: 96  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-220-528-15

Query Match 58.9%; Score 511; DB 4; Length 156;  
Best Local Similarity 64.2%; Pred. No. 1e-50;  
Matches 102; Conservative 16; Mismatches 35; Indels 6; Gaps 3;  
Patent No. 6284540  
GENERAL INFORMATION:  
APPLICANT: Milbrandt, Jeffrey D.  
APPLICANT: Baloh, Robert H.  
TITLE OF INVENTION: Artemin, A No. 6284540el Neurotrophic Factor  
FILE REFERENCE: 6029-7998  
CURRENT APPLICATION NUMBER: US/09/220,528A  
CURRENT FILING DATE: 1998-12-24  
EARLIER APPLICATION NUMBER: 09/218,698  
EARLIER FILING DATE: 1998-12-22  
EARLIER APPLICATION NUMBER: 60/108,148  
EARLIER FILING DATE: 1998-11-12  
EARLIER APPLICATION NUMBER: 09/163,283  
EARLIER FILING DATE: 1998-09-29  
NUMBER OF SEQ ID NOS: 120  
SEQ ID NO 15  
LENGTH: 96  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-220-528-15

Query Match 58.9%; Score 511; DB 4; Length 156;  
Best Local Similarity 64.2%; Pred. No. 1e-50;  
Matches 102; Conservative 16; Mismatches 35; Indels 6; Gaps 3;  
Patent No. 6284540  
GENERAL INFORMATION:  
APPLICANT: Milbrandt, Jeffrey D.  
APPLICANT: Baloh, Robert H.  
TITLE OF INVENTION: Artemin, A No. 6284540el Neurotrophic Factor  
FILE REFERENCE: 6029-7998  
CURRENT APPLICATION NUMBER: US/09/220,528A  
CURRENT FILING DATE: 1998-12-24  
EARLIER APPLICATION NUMBER: 09/218,698  
EARLIER FILING DATE: 1998-12-22  
EARLIER APPLICATION NUMBER: 60/108,148  
EARLIER FILING DATE: 1998-11-12  
EARLIER APPLICATION NUMBER: 09/163,283  
EARLIER FILING DATE: 1998-09-29  
NUMBER OF SEQ ID NOS: 120  
SEQ ID NO 15  
LENGTH: 96  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-220-528-15

Query Match 58.9%; Score 511; DB 4; Length 156;  
Best Local Similarity 64.2%; Pred. No. 1e-50;  
Matches 102; Conservative 16; Mismatches 35; Indels 6; Gaps 3;  
Patent No. 6284540  
GENERAL INFORMATION:  
APPLICANT: Milbrandt, Jeffrey D.  
APPLICANT: Baloh, Robert H.  
TITLE OF INVENTION: Artemin, A No. 6284540el Neurotrophic Factor  
FILE REFERENCE: 6029-7998  
CURRENT APPLICATION NUMBER: US/09/220,528A  
CURRENT FILING DATE: 1998-12-24  
EARLIER APPLICATION NUMBER: 09/218,698  
EARLIER FILING DATE: 1998-12-22  
EARLIER APPLICATION NUMBER: 60/108,148  
EARLIER FILING DATE: 1998-11-12  
EARLIER APPLICATION NUMBER: 09/163,283  
EARLIER FILING DATE: 1998-09-29  
NUMBER OF SEQ ID NOS: 120  
SEQ ID NO 15  
LENGTH: 96  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-220-528-15

**RESULT 7**  
 Sequence 223, Application US/08931858E  
 Patent No. 622022  
 GENERAL INFORMATION:  
 APPLICANT: JOHNSON, EUGENE M  
 APPLICANT: MILBRANDT, JEFFREY D  
 APPLICANT: KOTZBAUER, PAUL T  
 APPLICANT: LAMPE, PATRICIA A  
 APPLICANT: KLEIN, ROBERT  
 APPLICANT: DESAUVAGE, FRED  
 TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTOR  
 NUMBER OF SEQUENCES: 239  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: HOWELL & HAERKAMP, L.C.  
 STREET: 7733 FORSYTH BOULEVARD, SUITE 1400  
 CITY: ST. LOUIS  
 STATE: MO  
 ZIP: 63105  
 COMPUTER READABLE FORM:  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/931,858E  
 FILING DATE:  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: HOLLAND, DONALD R.  
 REGISTRATION NUMBER: 35,197  
 REFERENCE/DOCKET NUMBER: 971486  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 314-727-6092  
 TELEFAX: 314-727-5188  
 INFORMATION FOR SEQ ID NO: 223:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 89 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-931-858E-223

Query Match 58.6%; Score 492; DB 4; Length 89;  
 Best Local Similarity 100.0%; Pred. No. 7.3e-49;  
 Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 66 CQLWSLTVAELGLGYSBEKIVFRYCAASPRGARTQHGLALARQOGRAHGGPCCR 125  
 Db 1 CQLWSLTVAELGLGYSBEKIVFRYCAASPRGARTQHGLALARQOGRAHGGPCCR 60

Qy 126 PTRYTDVAFLDRHRWQLPQLSAAACGC 154  
 Db 61 PTRYTDVAFLDRHRWQLPQLSAAACGC 89

**RESULT 8**  
 Sequence 18, Application US/09220528A  
 Patent No. 6224540  
 GENERAL INFORMATION:  
 APPLICANT: Milbrandt, Jeffrey D.  
 APPLICANT: Baloh, Robert H.  
 TITLE OF INVENTION: Artemin, A No. 6284540e1 Neurotrophic Factor  
 FILE REFERENCE: 609-798  
 CURRENT APPLICATION NUMBER: US/09/220,528A  
 CURRENT FILING DATE: 1998-12-24  
 EARLIER APPLICATION NUMBER: 09/218,698  
 EARLIER FILING DATE: 1998-12-22

EARLIER APPLICATION NUMBER: 60/108,149  
 EARLIER FILING DATE: 1998-11-12  
 EARLIER APPLICATION NUMBER: 09/163,283  
 NUMBER OF SEQ ID NOS: 120  
 SOFTWARE: Patentin Ver. 2.0  
 SEQ ID NO: 18  
 LENGTH: 89  
 TYPE: PRT  
 ORGANISM: HOMO sapiens  
 US-09-220-528-18

Query Match 58.6%; Score 492; DB 4; Length 89;  
 Best Local Similarity 100.0%; Pred. No. 7.3e-49;  
 Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 66 CQLWSLTVAELGLGYSBEKIVFRYCAASPRGARTQHGLALARQOGRAHGGPCCR 125  
 Db 1 CQLWSLTVAELGLGYSBEKIVFRYCAASPRGARTQHGLALARQOGRAHGGPCCR 60

Qy 126 PTRYTDVAFLDRHRWQLPQLSAAACGC 154  
 Db 61 PTRYTDVAFLDRHRWQLPQLSAAACGC 89

RESULT 9  
 US-08-981-739-133  
 Sequence 133, Application US/08981739  
 Patent No. 6232449

GENERAL INFORMATION:  
 APPLICANT: JOHNSON JR., EUGENE M.  
 MILEBRANDT, JEFFREY D.  
 KOTZBAUER, PAUL T.  
 LAMPE, PATRICIA A.

TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTORS  
 NUMBER OF SEQUENCES: 176  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: HOWELL & HAERKAMP, L.C.  
 STREET: 7733 FORSYTH BOULEVARD, SUITE 1400  
 CITY: ST. LOUIS  
 STATE: MISSOURI  
 COUNTRY: US  
 ZIP: 63105-1817

COMPUTER READABLE FORM:  
 MEDIUM TYPE: FLOPPY disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/981,739  
 FILING DATE: 31-Aug-1998  
 CLASSIFICATION: <Unknown>  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US97/03461  
 FILING DATE: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: HOLLAND, DONALD R.  
 REGISTRATION NUMBER: 35,197  
 REFERENCE/DOCKET NUMBER: 971663  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (314) 727-5188  
 TELEFAX: (314) 727-6092  
 INFORMATION FOR SEQ ID NO: 133:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 185 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-981-739-133

Query Match 53.9%; Score 452; DB 4; Length 185;

Best Local Similarity 57.3%; Pred. No. 6.7e-44; Matches 94; Conservative 14; Mismatches 40; Indels 16; Gaps 3;

Qy 9 GSLL-----LSQLG-----QWGPNDAR----GVPADGEFSSEQVAKAGGTWLCTH 52  
 1|||:  
 Db 22 GSLLFKRLWQISSHLGRWLEGPGRPIVRVPGGLPTPQFLSKPSCLTLLYLALG 81

Qy 53 RPLARLRLASGPOLMSLTLVAELGLYASEEKVIFRYCAGSCPRGARTQHGLALARL 112  
 1|||:  
 Db 82 NHVRLPLALGSCLRWLSLTPVAEGLYASEEVIFRYCAGSCPRGARTQHSLYLALR 141

Qy 113 QGOGRAHGPCCPRTYDVAFLDDRHWRQLPQLSAAACGGG 156  
 1|||:  
 Db 142 RGRGRAHGPCCPQPTSYADVTFLDDOHMWWQLPQLSAAACGGG 185

RESULT 10  
 US-09-128-026-133  
 Sequence 133, Application US/09128026  
 Parent No. 640335

GENERAL INFORMATION:

APPLICANT: JOHNSON JR., EUGENE M.  
 ATTORNEY/AGENT INFORMATION:  
 NAME: KOTZBAUER, PAUL D.

APPLICANT: MILBRANDT, JEFFREY D.  
 ATTORNEY/AGENT INFORMATION:  
 NAME: HAFERKAMP, L.C.

APPLICANT: LAMPE, PATRICIA A.  
 ATTORNEY/AGENT INFORMATION:  
 NAME: HOWELL & HAVERKAMP, L.C.

NUMBER OF SEQUENCES: 176  
 NUMBER OF SEQUENCES: 176

CORRESPONDENCE ADDRESS:

ADDRESSEE: HOWELL & HAVERKAMP, L.C.  
 STREET: 7733 FORSYTH BOULEVARD, SUITE 1400  
 CITY: ST. LOUIS  
 STATE: MISSOURI  
 COUNTRY: US  
 ZIP: 63105-1817

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/128,026  
 FILING DATE: 09-Nov-2002  
 PRIORITY DATE: 09-Nov-2002  
 REFERENCE/DOCKET NUMBER: 976163

ATTORNEY/AGENT INFORMATION:

NAME: HOLLAND, DONALD R.  
 REGISTRATION NUMBER: 35,197  
 REFERENCE/DOCKET NUMBER: 976163

TELECOMMUNICATION INFORMATION:

TELEPHONE: (314) 727-5188  
 TELEFAX: (314) 727-5188

INFORMATION FOR SEQ ID NO: 81:

SEQUENCE CHARACTERISTICS:

SEQUENCE DESCRIPTION: SEQ ID NO: 81:  
 US-08-981-739-81

Query Match 53.8%; Score 452; DB 4; Length 134;  
 Best Local Similarity 81.0%; Pred. No. 5.8e-44; Mismatches 8; Indels 0; Gaps 0;

Qy 57 RLRRRLSGPCQWLSLTSVAVELGLYASBEKVIFRYCAGSCPRGARTQHGLALARQG 116  
 1|||:  
 Db 35 RLPLAIGSCLRWLSLTPVAEGLYASEEVIFRYCAGSCPRGARTQHSLYLALR 94

Qy 117 RAHGGPCCRPRTYDVAFLDDRHWRQLPQLSAAACGGG 156  
 1|||:  
 Db 95 RAHGRGPCCPQPTSYADVTFLDDOHMWWQLPQLSAAACGGG 134

RESULT 12  
 US-08-981-026-81  
 Sequence 81, Application US/09128026  
 Patent No. 640335

GENERAL INFORMATION:

APPLICANT: JOHNSON JR., EUGENE M.  
 ATTORNEY/AGENT INFORMATION:  
 NAME: KOTZBAUER, PAUL D.

APPLICANT: MILBRANDT, JEFFREY D.  
 ATTORNEY/AGENT INFORMATION:  
 NAME: HAFERKAMP, L.C.

APPLICANT: LAMPE, PATRICIA A.  
 ATTORNEY/AGENT INFORMATION:  
 NAME: HOWELL & HAVERKAMP, L.C.

NUMBER OF SEQUENCES: 176  
 NUMBER OF SEQUENCES: 176

CORRESPONDENCE ADDRESS:

ADDRESSEE: HOWELL & HAVERKAMP, L.C.  
 STREET: 7733 FORSYTH BOULEVARD, SUITE 1400  
 CITY: ST. LOUIS  
 STATE: MISSOURI  
 COUNTRY: US  
 ZIP: 63105-1817

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/128,026  
 FILING DATE: 09-Nov-2002  
 PRIORITY DATE: 09-Nov-2002  
 REFERENCE/DOCKET NUMBER: 976163

ATTORNEY/AGENT INFORMATION:

NAME: HOLLAND, DONALD R.  
 REGISTRATION NUMBER: 35,197  
 REFERENCE/DOCKET NUMBER: 976163

TELECOMMUNICATION INFORMATION:

TELEPHONE: (314) 727-5188  
 TELEFAX: (314) 727-6092

INFORMATION FOR SEQ ID NO: 133:

SEQUENCE CHARACTERISTICS:

SEQUENCE DESCRIPTION: SEQ ID NO: 81:  
 US-08-981-739-81

Query Match 53.9%; Score 452; DB 4; Length 185;  
 Best Local Similarity 57.3%; Pred. No. 6.7e-44;  
 Matches 94; Conservative 14; Mismatches 40; Indels 16; Gaps 3;

Qy 9 GSLL-----LSQLG-----QWGPNDAR----GVPADGEFSSEQVAKAGGTWLCTH 52  
 1|||:  
 Db 22 GSLLFKRLWQISSHLGRWLEGPGRPIVRVPGGLPTPQFLSKPSCLTLLYLALG 81

Qy 53 RPLARLRLASGPOLMSLTLVAELGLYASEEVIFRYCAGSCPRGARTQHGLALARL 112  
 1|||:  
 Db 82 NHVRLPLALGSCLRWLSLTPVAEGLYASEEVIFRYCAGSCPRGARTQHSLYLALR 141

Qy 113 QGOGRAHGPCCPRTYDVAFLDDRHWRQLPQLSAAACGGG 156  
 1|||:  
 Db 142 RGRGRAHGPCCPQPTSYADVTFLDDOHMWWQLPQLSAAACGGG 134

GENERAL INFORMATION:

APPLICANT: JOHNSON JR., EUGENE M.  
 ATTORNEY/AGENT INFORMATION:  
 NAME: KOTZBAUER, PAUL D.

APPLICANT: MILBRANDT, JEFFREY D.  
 ATTORNEY/AGENT INFORMATION:  
 NAME: HAFERKAMP, L.C.

APPLICANT: LAMPE, PATRICIA A.  
 ATTORNEY/AGENT INFORMATION:  
 NAME: HOWELL & HAVERKAMP, L.C.

NUMBER OF SEQUENCES: 176  
 NUMBER OF SEQUENCES: 176

CORRESPONDENCE ADDRESS:

ADDRESSEE: HOWELL & HAVERKAMP, L.C.  
 STREET: 7733 FORSYTH BOULEVARD, SUITE 1400  
 CITY: ST. LOUIS  
 STATE: MISSOURI  
 COUNTRY: US  
 ZIP: 63105-1817

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/128,026  
 FILING DATE: 09-Nov-2002  
 PRIORITY DATE: 09-Nov-2002  
 REFERENCE/DOCKET NUMBER: 976163

ATTORNEY/AGENT INFORMATION:

NAME: HOLLAND, DONALD R.  
 REGISTRATION NUMBER: 35,197  
 REFERENCE/DOCKET NUMBER: 976163

TELECOMMUNICATION INFORMATION:

TELEPHONE: (314) 727-5188  
 TELEFAX: (314) 727-6092

INFORMATION FOR SEQ ID NO: 133:

SEQUENCE CHARACTERISTICS:

SEQUENCE DESCRIPTION: SEQ ID NO: 81:  
 US-08-981-739-81

Query Match 53.8%; Score 452; DB 4; Length 134;  
 Best Local Similarity 81.0%; Pred. No. 5.8e-44; Mismatches 8; Indels 0; Gaps 0;

Qy 57 RLRRRLSGPCQWLSLTSVAVELGLYASBEKVIFRYCAGSCPRGARTQHGLALARQG 116  
 1|||:  
 Db 35 RLPLAIGSCLRWLSLTPVAEGLYASEEVIFRYCAGSCPRGARTQHSLYLALR 94

Qy 117 RAHGGPCCRPRTYDVAFLDDRHWRQLPQLSAAACGGG 156  
 1|||:  
 Db 95 RAHGRGPCCPQPTSYADVTFLDDOHMWWQLPQLSAAACGGG 134

GENERAL INFORMATION:

APPLICANT: JOHNSON JR., EUGENE M.  
 ATTORNEY/AGENT INFORMATION:  
 NAME: KOTZBAUER, PAUL D.

APPLICANT: MILBRANDT, JEFFREY D.  
 ATTORNEY/AGENT INFORMATION:  
 NAME: HAFERKAMP, L.C.

APPLICANT: LAMPE, PATRICIA A.  
 ATTORNEY/AGENT INFORMATION:  
 NAME: HOWELL & HAVERKAMP, L.C.

NUMBER OF SEQUENCES: 176  
 NUMBER OF SEQUENCES: 176

CORRESPONDENCE ADDRESS:

ADDRESSEE: HOWELL & HAVERKAMP, L.C.  
 STREET: 7733 FORSYTH BOULEVARD, SUITE 1400  
 CITY: ST. LOUIS  
 STATE: MISSOURI  
 COUNTRY: US  
 ZIP: 63105-1817

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/128,026  
 FILING DATE: 09-Nov-2002  
 PRIORITY DATE: 09-Nov-2002  
 REFERENCE/DOCKET NUMBER: 976163

ATTORNEY/AGENT INFORMATION:

NAME: HOLLAND, DONALD R.  
 REGISTRATION NUMBER: 35,197  
 REFERENCE/DOCKET NUMBER: 976163

TELECOMMUNICATION INFORMATION:

TELEPHONE: (314) 727-5188  
 TELEFAX: (314) 727-6092

INFORMATION FOR SEQ ID NO: 133:

SEQUENCE CHARACTERISTICS:

SEQUENCE DESCRIPTION: SEQ ID NO: 81:  
 US-08-981-739-81

Query Match 53.9%; Score 452; DB 4; Length 185;  
 Best Local Similarity 57.3%; Pred. No. 6.7e-44;  
 Matches 94; Conservative 14; Mismatches 40; Indels 16; Gaps 3;

Qy 9 GSLL-----LSQLG-----QWGPNDAR----GVPADGEFSSEQVAKAGGTWLCTH 52  
 1|||:  
 Db 22 GSLLFKRLWQISSHLGRWLEGPGRPIVRVPGGLPTPQFLSKPSCLTLLYLALG 81

Qy 53 RPLARLRLASGPOLMSLTLVAELGLYASEEVIFRYCAGSCPRGARTQHGLALARL 112  
 1|||:  
 Db 82 NHVRLPLALGSCLRWLSLTPVAEGLYASEEVIFRYCAGSCPRGARTQHSLYLALR 141

Qy 113 QGOGRAHGPCCPRTYDVAFLDDRHWRQLPQLSAAACGGG 156  
 1|||:  
 Db 142 RGRGRAHGPCCPQPTSYADVTFLDDOHMWWQLPQLSAAACGGG 134



Search completed: July 11, 2003, 12:48:23  
 Job time : 14 secs

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**RESULT 15**

Query Match 53.8%; Score 451; DB 4; Length 142;  
 Best Local Similarity 81.0%; Pred. No. 6.2e-44;  
 Matches 81; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

Qy 57 RLRRALSGPCOLWSLTLVAFLGLYASPERVIFRCAGGSCPQARTQGLALARLOGQ 116  
 Db 43 RLPRALAGSCRWLSPVAAEGLYASEEPKVIRYCAGSCPQARTQHSLVLARLRGRG 102

Qy 117 RAHGGPCCRPTRTDVAFLDRHRWQLSAAACGGG 156  
 Db 103 RAHGPCCCPQTSYADYTFDDHHWQQLPQLSAAACGGG 142

**RESULT 15**

Sequence 111; Application US/09128026  
 Patent No. 640335

**GENERAL INFORMATION:**

APPLICANT: JOHNSON JR., EUGENE M.  
 MILBRANDT, JEFFREY D.  
 KOTZBAUER, PAUL T.

APPLICANT: LAMPE, PATRICIA A.

TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTORS

NUMBER OF SEQUENCES: 176

CORRESPONDENCE ADDRESS:

ADDRESSEE: HOWELL & HAERKAMP, L.C.  
 STREET: 7733 FORSTH BOULEVARD, SUITE 1400  
 CITY: ST. LOUIS  
 STATE: MISSOURI  
 COUNTRY: US  
 ZIP: 63105-1817

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09128,026

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: HOLLAND, DONALD R.  
 REGISTRATION NUMBER: 35,197  
 REFERENCE/DOCKET NUMBER: 97-163

TELECOMMUNICATION INFORMATION:

TELEPHONE: (314) 727-5188  
 TELEFAX: (314) 727-6092

INFORMATION FOR SEQ ID NO: 111:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 142 amino acids  
 TYPE: amino acid

STRANDEDNESS:  
 TOPOLOGY: linear

MOLECULE TYPE: protein

us-09-128-026-111

Query Match 53.8%; Score 451; DB 4; Length 142;  
 Best Local Similarity 81.0%; Pred. No. 6.2e-44;  
 Matches 81; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

Qy 57 RLRRALSGPCOLWSLTLVAFLGLYASPERVIFRCAGGSCPQARTQGLALARLOGQ 116  
 Db 43 RLPRALAGSCRWLSPVAAEGLYASEEPKVIRYCAGSCPQARTQHSLVLARLRGRG 102

Qy 117 RAHGGPCCRPTRTDVAFLDRHRWQLSAAACGGG 156  
 Db 103 RAHGPCCCPQTSYADYTFDDHHWQQLPQLSAAACGGG 142

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US-09-800-729-101 ; Sequence 101, Application US/09800729  
; Patent No. US2002006319A1  
; GENERAL INFORMATION:  
; APPLICANT: Ni et al.  
; TITLE OF INVENTION: 32 Human secreted proteins  
; FILE REFERENCE: P204A1  
; CURRENT APPLICATION NUMBER: US/09/800-729  
; CURRENT FILING DATE: 2001-03-08  
; PRIOR APPLICATION NUMBER: PCT/US00/26013  
; PRIOR FILING DATE: 2000-09-22  
; PRIOR APPLICATION NUMBER: 60/155,709  
; PRIOR FILING DATE: 1999-09-24  
; NUMBER OF SEQ ID NOS: 217  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO: 101  
; LENGTH: 183  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (86)  
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids  
; NAME/KEY: SITE  
; LOCATION: (146)  
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids  
; US-09-800-729-101  
Query Match 66.1%; Score 554.5%; DB 10; Length 183;  
Best Local Similarity 63.4%; Pred. No. 2,2e-44;  
Matches 118; Conservative 5; Mismatches 30; Indels 33; Gaps 5;  
Qy 1 MAVGKFLGSLLLISLQLQGMCPDARGVPVADGEFSSEQVAKAGGTWLGHTH---RPLA 56  
Db 1 MAVGFLGSLLLISLQLQGMCPDARGVPVADGEFSSEQVAKAGGTWLKGDPGSVTS 60  
Qy 57 RLRLRS-----GPCQLWSL-----TLYSAELGLGYASEEKVIF 90  
Db 61 QSPALTLLTVSALPSHRRHPPCPXAPSPWMPAVPDRVRGPGLRLIGE-VIF 118  
Qy 91 RYCAAGSCPGRGARTOHLGLALARLGQGRAHGGPCRCPTRYTDVAFLLDRHRWQLPOLSRA 150  
Db 119 RYCAAGSCPGRGARTOHLGLALARLGQGRAHGGPCRCPTRYTDVAFLLDRHRWQLPOLSRA 177  
Qy 151 AGCGGG 155  
Db 178 LGCGGG 183  
SULI<sup>3</sup>  
\*09-220-920-15  
Sequence 15, Application US/09220920  
; Patent No. US2002002269A1  
; GENERAL INFORMATION:  
; APPLICANT: Milbrandt, Jeffrey D.  
; TITLE OF INVENTION: Artemin, A No. US2002002269A1 Neurotrophic Factor  
; FILE REFERENCE: 6029-7996  
; CURRENT APPLICATION NUMBER: US/09/220-920  
; CURRENT FILING DATE: 1998-12-14  
; EARLIER APPLICATION NUMBER: 09/163,283  
; EARLIER FILING DATE: 1998-09-29  
; EARLIER APPLICATION NUMBER: 60/108,148  
; EARLIER FILING DATE: 1998-11-12  
; EARLIER APPLICATION NUMBER: 09/218,698  
; EARLIER FILING DATE: 1998-12-22  
; NUMBER OF SEQ ID NOS: 120  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO: 18  
; LENGTH: 89  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-220-920-18  
Query Match 58.6%; Score 492; DB 10; Length 89;  
Best Local Similarity 100.0%; Pred. No. 6,8e-39;  
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 66 QLNLSTLISLVAELGLGYASEEKVIFRVCAGSCSPRGARTOHLGLALARLGQGRAHGGPCCR 125  
Db 1 QLNLSLTISLVAELGLGYASEEKVIFRVCAGSCSPRGARTOHLGLALARLGQGRAHGGPCCR 60  
Qy 126 PTRTYDVAFLDRHRWQLPQLSAAAGC 154  
Db 61 PTRTYDVAFLDRHRWQLPQLSAAAGC 89  
RESULT 4  
US-09-220-920-18  
; Sequence 18, Application US/09220920  
; Patent No. US2002002269A1  
; GENERAL INFORMATION:  
; APPLICANT: Milbrandt, Jeffrey D.  
; TITLE OF INVENTION: Artemin, A No. US2002002269A1 Neurotrophic Factor  
; FILE REFERENCE: 6029-7996  
; CURRENT APPLICATION NUMBER: US/09/220-920  
; CURRENT FILING DATE: 1998-12-14  
; EARLIER APPLICATION NUMBER: 09/163,283  
; EARLIER FILING DATE: 1998-09-29  
; EARLIER APPLICATION NUMBER: 60/108,148  
; EARLIER FILING DATE: 1998-11-12  
; EARLIER APPLICATION NUMBER: 09/218,698  
; EARLIER FILING DATE: 1998-12-22  
; NUMBER OF SEQ ID NOS: 120  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO: 18  
; LENGTH: 89  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; US-09-220-920-18  
Query Match 58.6%; Score 492; DB 10; Length 89;  
Best Local Similarity 100.0%; Pred. No. 6,8e-39;  
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 66 QLNLSTLISLVAELGLGYASEEKVIFRVCAGSCSPRGARTOHLGLALARLGQGRAHGGPCCR 125  
Db 1 QLNLSLTISLVAELGLGYASEEKVIFRVCAGSCSPRGARTOHLGLALARLGQGRAHGGPCCR 60  
Qy 126 PTRTYDVAFLDRHRWQLPQLSAAAGC 154  
Db 61 PTRTYDVAFLDRHRWQLPQLSAAAGC 89  
RESULT 5  
US-09-800-729-133  
; Sequence 133, Application US/09800729  
; Patent No. US2002006319A1  
; GENERAL INFORMATION:  
; APPLICANT: Ni et al.  
; TITLE OF INVENTION: 32 Human secreted proteins  
; FILE REFERENCE: P204A1  
; CURRENT APPLICATION NUMBER: US/09/800-729  
; CURRENT FILING DATE: 2001-03-08  
; PRIOR APPLICATION NUMBER: PCT/US00/26013  
; PRIOR FILING DATE: 2000-09-22  
; PRIOR APPLICATION NUMBER: 60/155,709  
; PRIOR FILING DATE: 1999-09-24  
; NUMBER OF SEQ ID NOS: 217  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO: 133  
; LENGTH: 252  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; US-09-220-920-15

; NAME/KEY: SITE  
; LOCATION: (86)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; LOCATION: (116)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; LOCATION: (135)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; NAME/KEY: SITE  
; LOCATION: (146)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-09-800-729-133

Query Match Score 294; DB 10; Length 252;  
Best Local Similarity 41.6%; Pred. No. 6.7e-20;  
Matches 87; Conservative 8; Mismatches 50; Indels 64; Gaps 8;  
Qy 1 MAYGKFLIGSLLSSLQLGQSGWPDARGYPVADEGEFSSEQVAKAGGTWLGTH---RPLA 56  
Db 1 MAYGKFLIGSLLSSLQLGQSGWPDARGYPVADEGEFSSEQVAKAGGTWLGKDQGP SVTS 60  
Qy 57 RFLRLRS-----GPECOLWSL-----TILSVAEELGLGYASEE--KV 88  
Db 61 QLSPLAHTLYSALPSHRHPPCPXPSPDWNSPAVEDPDPYGRAPGRLIGEXHLPL 120  
Qy 89 IFPYCAGSCPRQARTQHGLALARLQOGRAHGGFCCCRPTRYTVAFLDDRH----RW 141  
Db 121 LRQOLPPWCPHFA-----WAGAGPA-AFGGPXPZRALLPAHSLHRRQLPQQPRW 169  
Qy 142 QRLPQLSAA-----ACGGGG 156  
Db 170 QRLPQLSAALRWWLRVPLAPRSCAGG 198

RESULT 6  
; Sequence 5 Application US/09220920  
; Patent No. US20020002269A1  
; GENERAL INFORMATION:  
; APPLICANT: Milbradt, Jeffrey D.  
; ; APPLICANT: Baloh, Robert H.  
; TITLE OF INVENTION: Attentin, A. NO. US20020002269A1el Neurotrophic Factor  
; FILE REFERENCE: 6029-7916  
; CURRENT APPLICATION NUMBER: US/09/220,920  
; CURRENT FILING DATE: 1998-12-24  
; EARLIER APPLICATION NUMBER: 09/163,283  
; EARLIER FILING DATE: 1998-09-29  
; EARLIER APPLICATION NUMBER: 60/108,148  
; EARLIER FILING DATE: 1998-11-12  
; EARLIER APPLICATION NUMBER: 09/218,698  
; EARLIER FILING DATE: 1998-12-22  
; NUMBER OF SEQ ID NOS: 120  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 140  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-220-920-5

Query Match Score 244; DB 10; Length 140;  
Best Local Similarity 44.8%; Pred. No. 1.7e-15;  
Matches 56; Conservative 17; Mismatches 36; Indels 16; Gaps 3;  
Qy 40 QVAKAGGTWLGTHPLRLRRLAQLGPQLWSLTUSVAELGLGYASEEKFVRYCAGSCPR 99  
Db 24 RAARAGG-----PGSRAAAGARGCRLRSQVLVPVRAALGHSDELVRFCSSC-R 75  
Qy 100 GARTQHGLALARLQOGG-----RAHGGPCCRPTRYTVAFLDDRRHWRQPLSAAA 151  
Db 76 RARSPHDLSSLIGAGALRPQPGSRPVSQCCRPTREAVSMFDVNSTWRTVDRLSATA 135  
Qy 152 CGGGG 156  
Db 136 CGCLG 140

RESULT 8  
US-09-220-920-12  
; Sequence 12, Application US/09220920  
; Patent No. US20020002269A1  
; GENERAL INFORMATION:  
; APPLICANT: Milbradt, Jeffrey D.  
; ; APPLICANT: Baloh, Robert H.  
; TITLE OF INVENTION: Attentin, A. NO. US20020002269A1el Neurotrophic Factor  
; FILE REFERENCE: 6029-7916  
; CURRENT APPLICATION NUMBER: US/09/220,920  
; CURRENT FILING DATE: 1998-12-24  
; EARLIER APPLICATION NUMBER: 09/163,283  
; EARLIER FILING DATE: 1998-09-29  
; EARLIER APPLICATION NUMBER: 60/108,148  
; EARLIER FILING DATE: 1998-11-12  
; NUMBER OF SEQ ID NOS: 120  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 140  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-220-920-5

Query Match Score 2918; DB 10; Length 140;  
Best Local Similarity 44.8%; Pred. No. 1.7e-15;  
Matches 56; Conservative 17; Mismatches 36; Indels 16; Gaps 3;  
Qy 40 QVAKAGGTWLGTHPLRLRRLAQLGPQLWSLTUSVAELGLGYASEEKFVRYCAGSCPR 99  
Db 24 RAARAGG-----PGSRAAAGARGCRLRSQVLVPVRAALGHSDELVRFCSSC-R 75  
Qy 100 GARTQHGLALARLQOGG-----RAHGGPCCRPTRYTVAFLDDRRHWRQPLSAAA 151  
Db 76 RARSPHDLSSLIGAGALRPQPGSRPVSQCCRPTREAVSMFDVNSTWRTVDRLSATA 135  
Qy 152 CGGGG 156  
Db 136 CGCLG 140

RESULT 7  
US-09-804-615-10  
; Sequence 10, Application US/09804615  
; Patent No. US20020055467A1  
; GENERAL INFORMATION:  
; APPLICANT: Johansen, Teit E.  
; ; APPLICANT: Wen-Yee Saw, Dinah  
; TITLE OF INVENTION: No. US20020055467A1el Neurotrophic Factors  
; CURRENT APPLICATION NUMBER: US/09/804,615  
; CURRENT FILING DATE: 2001-03-12  
; PRIOR APPLICATION NUMBER: DANISH 1998 00904  
; PRIOR FILING DATE: 1998-07-06  
; PRIOR APPLICATION NUMBER: US/N 60/092,229  
; PRIOR FILING DATE: 1998-07-09  
; PRIOR APPLICATION NUMBER: DANISH 1998 01048  
; PRIOR FILING DATE: 1998-08-19  
; PRIOR APPLICATION NUMBER: US/N 60/097,774  
; PRIOR FILING DATE: 1998-08-25  
; PRIOR APPLICATION NUMBER: US/N 60/103,908  
; PRIOR FILING DATE: 1998-10-13  
; PRIOR APPLICATION NUMBER: DANISH 1998 01265  
; PRIOR FILING DATE: 1998-10-06  
; PRIOR APPLICATION NUMBER: U.S.S.N 09/347,613  
; PRIOR FILING DATE: 1999-07-02  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 10  
; LENGTH: 140  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE: CARBOHYD  
; NAME/KEY: LOCATION: (122)  
; OTHER INFORMATION: glycosylated asparagine  
US-09-804-615-10

Query Match Score 2918; DB 10; Length 140;  
Best Local Similarity 44.8%; Pred. No. 1.7e-15;  
Matches 56; Conservative 17; Mismatches 36; Indels 16; Gaps 3;  
Qy 40 QVAKAGGTWLGTHPLRLRRLAQLGPQLWSLTUSVAELGLGYASEEKFVRYCAGSCPR 99  
Db 24 RAARAGG-----PGSRAAAGARGCRLRSQVLVPVRAALGHSDELVRFCSSC-R 75  
Qy 100 GARTQHGLALARLQOGG-----RAHGGPCCRPTRYTVAFLDDRRHWRQPLSAAA 151  
Db 76 RARSPHDLSSLIGAGALRPQPGSRPVSQCCRPTREAVSMFDVNSTWRTVDRLSATA 135  
Qy 152 CGGGG 156  
Db 136 CGCLG 140

RESULT 8  
US-09-220-920-12  
; Sequence 12, Application US/09220920  
; Patent No. US20020002269A1  
; GENERAL INFORMATION:  
; APPLICANT: Milbradt, Jeffrey D.  
; ; APPLICANT: Baloh, Robert H.  
; TITLE OF INVENTION: Attentin, A. NO. US20020002269A1el Neurotrophic Factor  
; FILE REFERENCE: 6029-7916  
; CURRENT APPLICATION NUMBER: US/09/220,920  
; CURRENT FILING DATE: 1998-12-24  
; EARLIER APPLICATION NUMBER: 09/163,283  
; EARLIER FILING DATE: 1998-09-29  
; EARLIER APPLICATION NUMBER: 60/108,148  
; EARLIER FILING DATE: 1998-11-12  
; EARLIER APPLICATION NUMBER: 09/218,698  
; EARLIER FILING DATE: 1998-12-22  
; NUMBER OF SEQ ID NOS: 120  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 140  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-220-920-5



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**OM protein - protein search, using sw model**

Run on: July 11, 2003, 12:45:38 ; Search time 18 Seconds  
(without alignments)  
833.165 Million cell updates/sec

Title: US-09-220-617B-217

Perfect score: 839

Sequence: 1 MAVGKFLISLLSLQGQ.....DRHRWQRLPOLSAAAACGGG 156

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%  
Listing first 45 summaries

Database : PIR\_73:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	231.5	27.6	197	2	T47159		hypothetical prote
2	177.5	21.2	211	2	A49686		glial cell line-de
3	176.5	21.0	211	2	A37499		glial cell line-de
4	171	20.4	211	2	B37499		glial cell line-de
5	116.5	13.9	275	1	WF005		mullerian inhibit
6	115	13.7	560	1	WFHUM		mullerian inhibit
7	112	13.3	555	1	S20100		mullerian inhibit
8	110.5	13.2	553	1	A42499		mullerian inhibit
9	108.5	12.9	575	2	T11753		anti-mullerian hor
10	104	12.4	644	2	JC2466		activin - C pre
11	99	11.9	352	2	JC2466		activin - beta C cha
12	99	11.8	373	2	PM0042		activin - fruit fly
13	87	10.4	352	2	ST0580		activin beta C pre
14	85	10.1	373	2	T12063		xSL protein - Xan
15	84	10.0	352	2	JC5366		activin beta C - m
16	84	10.0	402	2	A83398		probable MFS trans
17	83.5	10.0	115	2	PN0396		activin beta B-2 C
18	83.5	10.0	393	2	I50103		activin beta B - z
19	83	10.0	467	1	KCHUN		neutrophil collage
20	82	9.8	370	2	F95363		probable serine-py
21	81.5	9.7	207	2	S3707		vgr protein - rat
22	81.5	9.7	255	2	I48235		inhibin beta-B cha
23	81.5	9.7	411	2	B41398		inhibin beta-B cha
24	81.5	9.7	510	2	A54798		Vg-1-related prote
25	81	9.7	408	1	BMHU4		bone morphogenetic
26	81	9.7	455	2	A43918		TGF-beta-related p
27	80.5	9.6	315	2	PN0505		activin beta B-1 C
28	80.5	9.6	349	1	WFPGBB		inhibin beta-B cha
29	80.5	9.6	407	1	A40150		inhibin beta-B cha

## ALIGNMENTS

RESULT 1	T47159	hypothetical protein DKFZp762B0211.1 - human
C;Species:	Homo sapiens (man)	
C;Date:	20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000	
R;Blum, H.; Bauersachs, S.; Mewes, H.W.; Weil, B.; Wiemann, S.		
submitted to the Protein Sequence Database, March 2000		
A;Reference number: 224379		
A;Accession: T47159		
A;Status: preliminary		
A;Molecule type: mRNA		
A;Residues: 1-197 <AAA>		
A;Cross references: EMBL:Ali61995		
A;Experimental source: adult melanoma (MeWo cell line); clone DKFZp762B0211		
C;Genetics:		
A;Note: DKFZp762B0211.1		
Query Match	27	6%
Best local Similarity	39.1%	DB 2;
Matches	68;	Conservative 15; Mismatches 56;
Indels	35;	Gaps 8;
QY	12	LLLSLQLGGGP-----DAR-----GVPVADGEFSSEQVAKAGGTWLG 51
Db	27	LLSHRLCPALVLPHLPLRTDLARLAQYRALLQQGAPDA---MELRELTWAGRPGP 83
QY	52	HR--PLARLRLASG--PCQLWSLTSVAELGLGYASEKVFRYCAAGSCPRGQHQG 106
Db	84	RRPAGPRERRARLARLARPCLGRELFRYCAAGSCAAARV-YD 142
QY	107	LALARLQ---GQGRAHGGPCCRPTRYD-VAFLDLDRWQLPQLSAAAGCG 154
Db	143	LGURRLRQRRLRURRERVRAQCCRPTAYEDEVSLDAHSRYHTWELSAECA 196
RESULT 2	I4986	glial cell line-derived neurotrophic factor - mouse
C;Species:	Mus musculus (house mouse)	
C;Date:	02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 08-Oct-1999	
C;Accession:	I49866; JC6558	
R;Watabe, K.; Fukuda, T.; Tanaka, J.; Honda, H.; Toyohara, K.; Sakai, O.		
J;Neurosci. Res. 41, 279-290, 1995		
A;Title: Spontaneous immortalized adult mouse Schwann cells secrete autocrine and p		
A;Reference number: 149686; PMID:9379105; PMID:7650763		
A;Accession: I49866		
A;Status: preliminary; translated from GB/EMBL/DBJ		
A;Molecule type: mRNA		
A;Residues: 1-211 <AAA>		
A;Cross references: GB:D49921; NID:9758584; PID:BA008660.1; PID:9758585		
R;Matsuishi, N.; Fujita, Y.; Tanaka, M.; Nogatsu, T.; Kiuchi, K.		
Gene 203, 149-157, 1997		

A; Title: Cloning and structural organization of the gene encoding the mouse glial cell line-derived neurotrophic factor precursor - rat  
 A; Reference number: JC6518; MUID:98086214; PMID:9426245  
 A; Accession: JCC518  
 A; Status: Preliminary  
 A; Molecule type: nucleic acid  
 A; Residues: 1-211 <HAT>

Query Match 21.2%; Score 177.5; DB 2; Length 211;  
 Best Local Similarity 34.6%; Pred. No. 1..e-09; Indels 9; Gaps 4;  
 Matches 47; Conservative 22; Mismatches 58; Indels 9; Gaps 4;

Qy 24 PDARGYPDAEFSSEQVAKAGGWTGLTHRPLRLRALSGPCQLMSLTSVAEGLGYA 83  
 Db 79 PRKQAAALPRERNQAAAASPENSRGKGR--RGQQGKNGCVLTAIHLNVTGLGYE 135  
 Qy 84 SKEVKIFRYCGSCPRGARTQHQGLALARQGQRAH---GGPCCRPTRY-TDVAFLDDR 138  
 Db 136 TKEELIFRYCGSC-ESAETMYDKILKNLSRSRRLTSDKGACCREVAFFDDLSFLDDN 194  
 Qy 139 HRWQRLPQLSAAACGC 154  
 Db 195 LVYHILRKHSKRCGC 210

RESULT 4

B7499  
 glial cell line-derived neurotrophic factor precursor - human  
 N; Alternate names: GDNF  
 C; Species: Homo sapiens (man)  
 C; Date: 26-Aug-1999 #sequence\_revision 26-Aug-1999 #text\_change 26-Aug-1999  
 C; Accession: B7499  
 R; Lin, L.F.; Doherty, D.H.; Lile, J.D.; Bektesh, S.; Collins, F.  
 C; Accession: A37499; 167605; I53427; I58180; S61537  
 R; Lin, L.F.; Doherty, D.H.; Lile, J.D.; Bektesh, S.; Collins, F.  
 Science 260, 1130-1132, 1993  
 A; Reference number: A37499; MUID:93262463; PMID:8493557  
 A; Title: GDNF, a glial cell line-derived neurotrophic factor for midbrain dopaminergic neurons  
 A; Reference number: A37499; MUID:93262463; PMID:8493557  
 A; Accession: A37499  
 A; Molecule type: mRNA; protein  
 A; Residues: 1-211 <LIN>  
 A; Cross-references: GB:U15305; PID:9310123; PIDN:AAA67909.1; PID:9310124  
 A; Experimental source: glial cell line B49  
 R; Springer, J.E.; Seeburger, J.L.; He, J.; Gabbe, A.; Blankenhorn, E.P.; Bergman, L.W.  
 Exp. Neurol. 131, 47-52, 1995  
 A; Title: cDNA sequence and differential mRNA regulation of two forms of glial cell line-derived neurotrophic factor  
 A; Reference number: I53427  
 A; Accession: I53427  
 A; Molecule type: mRNA; translated from GB/EMBL/DBJ  
 A; Cross-references: GB:S75583; PID:912788; PIDN:AA833B91.1; PID:9912789  
 A; Experimental source: strain uncertain; splice form GDNF633  
 R; Suter-Crazzolara, C.; Unsicker, K.  
 NeuroReport 5, 2486-2488, 1994  
 A; Title: GDNF is expressed in two forms in many tissues outside the CNS.  
 A; Reference number: 158180; MUID:95210610; PMID:7696586  
 A; Accession: I58180  
 A; Status: translated from GB/EMBL/DBJ  
 A; Molecule type: mRNA  
 A; Residues: 1-76, 'A'..52-76 <SUT>  
 A; Cross-references: EMBL:X92495; PID:9104219; PIDN:CAA63237.1; PID:9104220  
 A; Experimental source: strain Wistar; kidney  
 C; Genetics:  
 A; Gene: gdnf  
 C; Keywords: disulfide bond; glycoprotein; homodimer  
 F; 1-211/Product: glial cell line-derived neurotrophic factor splice form GDNF633 \*status  
 F; 1-211/Product: glial cell line-derived neurotrophic factor splice form GDNF633 \*status

RESULT 5

WFBO  
 muellerian inhibiting factor precursor - bovine  
 N; Alternate names: Mullerian Inhibiting substance (MIS)  
 C; Species: Bos primigenius taurus (cattle)  
 C; Date: 13-Aug-1986 #sequence\_revision 13-Aug-1986 #text\_change 01-Dec-2000  
 C; Accession: A01398; B01398  
 R; Caite, R.L.; Mattaliano, R.J.; Hession, C.; Mizard, R.; Farber, N.M.; Cheung, A.; Nian, K.L.; Rajin, R.C.; Mangano, T.F.; MacLaughlin, D.T.; Donahoe, P.K.  
 Cell 45, 685-698, 1986  
 A; Title: Isolation of the bovine and human genes for Muellerian inhibiting substance  
 A; Reference number: A90879; MUID:86216082; PMID:3754790  
 A; Accession: A01398  
 A; Molecule type: DNA  
 A; Residues: 1-14 <CAL>

A; Experimental source: newborn calf testis, clones cbm1915 and ps21

Scoring table:	BLOSUM62	
Gapop 10.0 , Gapext 0.5		
Searched:	112892 seqs, 41476328 residues	
Total number of hits satisfying chosen parameters:	112892	
Minimum DB seq length:	0	
Maximum DB seq length:	2000000000	
Post-processing:	Maximum Match 0% Listing first 45 summaries	
Database :	Swissprot_40 : *	
Pred. No.	is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	
SUMMARIES		
Result No.	Query Match Length DB ID	Description
1	839 100.0	060542 homo sapien
2	530 63.2	070301 rattus norvegicus
3	511 60.9	070300 musculus
4	231.5 27.6	099748 homo sapien
5	226.5 27.0	097463 musculus
6	177.5 21.2	045840 mus musculus
7	176.5 21.0	047731 rattus norvegicus
8	171 20.4	070395 homo sapien
9	116.5 13.9	030972 bos taurus
10	115 13.7	033711 homo sapien
11	112.5 13.4	092016 rattus norvegicus
12	112 13.3	027016 mus musculus
13	110.5 13.2	049000 rattus norvegicus
14	108.5 12.9	079295 sus scrofa
15	99.5 11.9	055103 homo sapien
16	94.5 11.3	092017 mus musculus
17	92 11.0	092015 rattus norvegicus
18	87 10.4	055104 mus musculus
19	86.5 10.3	092104 tricholium ciliatum
20	86.5 10.3	095390 homo sapien
21	84.5 10.1	018828 papio hamadryas
22	84 10.0	054778 agrobacterium
23	83.5 10.0	022894 homo sapien
24	82 9.8	043031 gallus gallus
25	82 9.8	026574 tribolium castaneum
26	82 9.8	048970 strongylocentrotus purpuratus
27	81.5 9.7	004906 rattus norvegicus
28	81.5 9.7	01HE9999 mus musculus
29	81.5 9.7	042222 brachydanio rerio
30	81.5 9.7	020722 mus musculus
31	81 9.7	012644 homo sapien
32	81 9.7	027091 drosophila melanogaster
33	80.5 9.6	040488 sus scrofa

ALIGNMENTS					
<b>RESULT</b> 1					
PSPN_HUMAN	ID	PSPN_HUMAN	STANDARD;	PRT;	156 AA.
AC	060542;				
DT	30-MAY-2000 (Rel. 39, Created)				
DT	30-MAY-2000 (Rel. 39, Last sequence update)				
DE	Persephin precursor (PSP).				
GN					
OS	Homo sapiens (Human).				
OC	Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; OC				
NCBI_TaxID=9606;					
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	PubMed=9491986;				
RA	Medline:98150950;				
RA	Millbrandt J., de Sauvage F.J., Fahrner T.J., Baloh R.H., Leitner M.L.,				
RA	Tansky M.G., Lampe P.A., Heuckeroth R.O., Fahrner T.J., Baloh R.H., Leitner M.L.,				
RA	Simburger K.S., Golden J.P., Davies J.A., Vejsada R., Kato A.C.,				
RA	Hynes M., Sherman D., Nishimura M., Wang L.-C., Vandlen R., Moffat B.,				
RA	Klein R.D., Poulsen K., Gray C., Garces A., Henderson C.E.,				
RA	Phillips H.S., Johnson E.M.;				
RT	"Persephin, a novel neurotrophic factor related to GDNF and				
RT	neurotrophin."				
RL	Neuron 20;245-253(1998).				
-I-	FUNCTION: EXHIBITS NEUROTROPHIC ACTIVITY ON MESENCEPHALIC				
CC	DOPAMINERGIC AND MOTOR NEURONS.				
CC	-I- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).				
CC	-I- SUBCELLULAR LOCATION: Secreted.				
CC	-I- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY. GDNF SUBFAMILY.				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).				
CC	EMBL: AF040962; AAC39640_1; -				
CC	HSSP: 007731; IAGC Genew: HGNC:9579; PSPN.				
CC	MM: 603921; InterPro: IPR001839; TGFB.				
DR	Pfam: PF00019; TGF-beta; 1.				
DR	SMART: SM00204; TGFB; 1.				
DR	PROSITE: PS00250; TGF-BETA_1; FALSE_NEG.				
KW	Growth factor; Signal.				
FT	POTENTIAL.				
FT	PERSEPHIN.				
FT	CHAIN.	22	156		
FT	DISULFID.	66	124		
FT	DISULFID.	93	152	BY SIMILARITY.	
FT	DISULFID.	97	154	BY SIMILARITY.	
FT	DISULFID.	123	123	BY SIMILARITY.	
SQ	SEQUENCE	156 AA;	16600 MW;	654751653A044A CRC44;	

Query Match	100.0%	Score 839;	DB 1;	Length 156;				
Best Local Similarity	100.0%	Pred. No. 3.2e-74;						
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;								
Qy	1	MAYGKFLIGSLLISLQLGQWGPARGPVADEGPSSSEQVAVAGGTWLGTHPLARLRR	60					
Db	1	MAYGKFLIGSLLISLQLGQWGPARGPVADEGPSSSEQVAVAGGTWLGTHPLARLRR	60					
Qy	61	ALSPCPQLSLTLVSABELGLYASEEKVYAGSCPRGARTQHGLALARLQGOGRAHG	120					
Db	61	ALSPCPQIWLWSLTSVAELGLYASEEKVYAGSCPRGARTQHGLALARLQGOGRAHG	120					
Qy	121	GPCCRPRTYTDVAFDDDRHWRQLRPLSAAACGCGG	156					
Db	121	GPCCRPRTYTDVAFDDDRHWRQLRPLSAAACGCGG	156					
<hr/>								
RESULT 2								
PSPN_RAT	ID	PSPN_RAT	STANDARD;	PRT;	156 AA.			
AC	OT0301;							
DT	30-MAY-2000	(Rel. 39. Created)						
DT	30-MAY-2000	(Rel. 39. Last sequence update)						
DT	16-OCT-2001	(Rel. 40. Last annotation update)						
DE	Persephin precursor (PSP).							
GN	PSPN.							
OS	Rattus norvegicus (Rat).							
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;							
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.							
OX	NCBI_TAXID=10116;							
RP	SEQUENCE FROM N.A.							
RX	MEDLINE-98130950;	PubMed=9491986;						
RA	Tansey M.G., de Sauvage P.A., Fahrner T.J., Baloh R.H., Leitner M.L.,							
RA	Malbrant J., Heucher R.O., Kotzbauer P.T.							
RA	Simburger K.S., Goldin J.P., Davies J.A., Vejsada R., Kato A.C.,							
RA	Hynes M., Sherman D., Nishimura M., Wang L.-C., Vandlen R., Moffat B.,							
RA	Klein R.D., Poulsen K., Gray C., Henderson C.E., Phillips H.S., Johnson E.M.;							
RT	"Persephin," a novel neurotrophic factor related to GDNF and							
RT	neurturin.							
RL	Neuron 20:245-253(1998).							
RN	[2]							
RP	SEQUENCE OF 1-78 FROM N.A.							
RC	STRAIN="prague-dawley"; TISSUE="pons";							
RX	MEDLINE=98374044; PubMed=710270;							
RA	Jaszai J., Parkas L.M., Galter D., Reuss B., Strelau J., Unsicker K., Kriegstein K.,							
RT	"GDNF"-related factor persephin is widely distributed throughout the nervous system."							
RL	J. Neurosci. Res. 53:494-501(1998).							
CC	-1- FUNCTION: EXHIBITS NEUROTROPHIC ACTIVITY ON MESENCEPHALIC DOPAMINERGIC AND MOTOR NEURONS.							
CC	-1- SUBUNIT: HOMODIMER; DISULFIDE LINKED (BY SIMILARITY).							
CC	-1- SUBUNIT: HOMODIMER; DISULFIDE LINKED (BY SIMILARITY).							
CC	-1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY. GDNF SUBFAMILY.							
CC	<hr/>							
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CC	EMBL; AF040961; AAC40058_1;							
DR	EMBL; AJ005169; CAA04010_1; -;							
DR	HSSP; Q07731; IAGO.							
DR	MGI; MGI:120168A; Pspn.							
DR	InterPro; IPR001839; TGFB.							
DR	PFAM; PF00119; TGF-beta_1.							
DR	SMART; SM00204; TGFB_1.							
DR	PROSITE; PS00250; TGF_BETA_1; FALSE_NEG.							
KW	Growth factor; Signal.							

FT	SIGNAL	1	21	POTENTIAL.
FT	CHAIN	22	156	PERSPHIN.
FT	DISULFID	66	124	BY SIMILARITY.
FT	DISULFID	93	152	BY SIMILARITY.
FT	DISULFID	97	154	BY SIMILARITY.
FT	DISULFID	123	123	INTERCHAIN (BY SIMILARITY).
SQ	SEQUENCE	156 AA:	17030 MW;	7D6DD813ZB041B CRC64;
Query	Match	60.9%	Score 511;	DB 1; Length 156;
Best	Local Similarity	64.2%	Pred. No. 1.5e-42;	
Matches	102;	Conservative	16;	Mismatches 35; Indels 6; Gaps 3;
Qy	1	MAVKFLGSLGSLLSLLQLGQWGPVAQDFSESEQVAKAGGTWL--GTHRLPLAR	57	
Qy	1	MAAGBLRLCLLCLLSPSLWLLQLEASVAD-KLSGPKMAETRWTQHGNIN--VR	57	
Qy	58	LRLALSGPCQLNLSLTSVAELGLGAYASEKEVTPRYCAGSCPRGARTQHGLALARQGQR	117	
Db	58	LPRALAGSCRMLNSLTLPEAEGLGASEKRVTPRYCAGSCPQEARIQHSLVLARLRGR	117	
Qy	118	AHGCGPCCRCRPTRTDVAFLDLDRHRQWRLPOLSSAACGGG	156	
Db	118	AHGRPPCCOPTSADYTFDQHHRQWRLPOLSSAACGGG	156	
<b>RESULT 4</b>				
ID	NRTN_HUMAN	STANDARD;	PRT;	197 AA.
AC	Q99748;			
DT	01-NOV-1997	(Rel. 35, Created)		
DT	01-NOV-1997	(Rel. 35, Last sequence update)		
DT	16-OCT-2001	(Rel. 40, Last annotation update)		
DE	Neurulin precursor.			
GN	NRTN.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OC	NCBI_TaxID=9606;			
RN	[1]	SEQUENCE FROM N.A.		
RP	RP	SEQUENCE FROM N.A.		
RX	RX	MEDLINE=>10100947; PubMed=8945474;		
RA	RA	Kottabauer P.T., Lampe P.A., Heuckeroth R.O., Golden J.P., Creedon D.J., Johnson E.M., Jr., Milbrandt J.J.,		
RA	RA	"Neurulin, a relative of glial-cell-line-derived neurotrophic factor."		
RT	RT	Hum. Mol. Genet. 7:1449-1452(1998).		
RL	RL	Nature 384:467-470(1996).		
RN	RN	[2]		
RP	RP	SEQUENCE FROM N.A.		
RC	RC	TISSUE=>Melanoma;		
RA	RA	Blum H., Bauerachs S., Newes H.-W., Weil B., Wiemann S., Doray B., Salomon R., Amiel J., Touraine R., Billaud M., Atlie T., Bachy B., Munich A., Lyonnet S.,		
RA	RA	"Mutation of the RET ligand, neurulin, supports multigenic inheritance in Hirschsprung disease."		
RT	RT	Hum. Mol. Genet. 7:1449-1452(1998).		
CC	CC	-1 FUNCTION: SUPPORTS THE SURVIVAL OF SYMPATHETIC NEURONS IN CULTURE.		
CC	CC	MAY REGULATE THE DEVELOPMENT AND MAINTENANCE OF THE CNS. MIGHT CONTROL THE SIZE OF NON-NEURONAL CELL POPULATION SUCH AS HAEMOPoietIC CELLS.		
CC	CC	-1 SUBUNIT: HOMODIMER; DISULFIDE-LINKED.		
CC	CC	-1 SUBCELLULAR LOCATION: Secreted.		
CC	CC	-1 DISEASE: IN ASSOCIATION WITH MUTATIONS OF RET GENE AND POSSIBLY OTHER LOCI, IT IS INVOLVED IN HIRSCHSPRUNG'S DISEASE (HSCR). THIS GENETIC DISORDER OF NEURAL CRIST DEVELOPMENT IS CHARACTERIZED BY THE ABSENCE OF INTRAMURAL GANGLION CELLS IN THE HINDGUT; OFTEN RESULTING IN INTESTINAL OBSTRUCTION.		
CC	CC	-1 SIMILARITY: BELONGS TO THE TGF-BETA FAMILY. GDNF SUBFAMILY.		

CC	MAY REGULATE THE DEVELOPMENT AND MAINTENANCE OF THE CNS. MIGHT CONTROL THE SIZE OF NON-NEURONAL CELL POPULATION SUCH AS HAEMOPOTIETIC CELLS.	RA	Watabe K., Fukuda T., Tanaka J., Honda H., Toyohara K., Sakai O.; "Spontaneously immortalized adult mouse Schwann cells secrete autocrine and paracrine growth-promoting activities.";
CC	- - SUBUNIT: HOMODIMER; DISULFIDE-LINKED.	RT	
CC	- - SUBCELLULAR LOCATION: Secreted.	RT	
CC	- - TISSUE/SPECIFICITY: WIDESPREAD DISTRIBUTION.	RL	J. Neurosci. Res. 41:279-290(1995).
CC	- - SIMILARITY: BELONGS TO THE TGFBETA FAMILY. GDNF SUBFAMILY.	RN	
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CC	EMBL: U78109; AAC52954.1; -.	RA	Matsuhashita N., Fujita Y., Nagatsu T., Klich K.; Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
CC	DR: Q07731; 1AGQ.	RL	Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
CC	DR: MGD: MG1:108417; NrtN.	CC	- - FUNCTION: NEUROTROPHIC FACTOR THAT ENHANCES SURVIVAL AND MORPHOLOGICAL DIFFERENTIATION OF DOPAMINERGIC NEURONS AND INCREASES THEIR HIGH-AFFINITY DOPAMINE UPTAKE.
CC	DR: InterPro: IPR002400; GF_cysknot.	CC	- - SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
CC	DR: InterPro: IPR001839; TGFB.	CC	- - SUBCELLULAR LOCATION: Secreted.
CC	DR: Pfam: PF0019; TGFB-beta; 1.	CC	- - ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC	DR: PRINTS: PRO0438; GFcysknot.	CC	- - SIMILARITY: BELONGS TO THE TGFBETA FAMILY. GDNF SUBFAMILY.
CC	DR: SMART: SM00204; TGFB; 1.	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.ebi-sib.ch/">http://www.ebi-sib.ch/</a> or send an email to license@ebi-sib.ch).
CC	DR: PROSITE: PS00250; TGFB_1; FALSE_NEG.	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.ebi-sib.ch/">http://www.ebi-sib.ch/</a> or send an email to license@ebi-sib.ch).
CC	DR: Growth factor; Signal; KW	CC	CC
FT	POTENTIAL.	CC	CC
FT	SIGNAL 1 19	CC	CC
FT	BY SIMILARITY.	CC	CC
FT	PROPEP 20 95	CC	CC
FT	BY SIMILARITY.	CC	CC
FT	CHAIN 95 195	CC	CC
FT	NEURUTIN.	CC	CC
FT	DISULFID 101 163	CC	CC
FT	BY SIMILARITY.	CC	CC
FT	DISULFID 128 192	CC	CC
FT	BY SIMILARITY.	CC	CC
FT	DISULFID 132 194	CC	CC
FT	BY SIMILARITY.	CC	CC
FT	DISULFID 162 162	CC	CC
FT	INTECHAIN [BY SIMILARITY].	CC	CC
SQ	DISULFID 195 AA: 22219 MW: ABB1B35D417448 CRC34;	CC	CC
CC	Query Match Best Local Similarity 27.0%; Score 226.5; DB 1; Length 195; Matches 68; Conservative 39.5%; Pred. No. 5./e-15; Indels 33; Gaps 8;	DR	DR: U37459; AAB18672.1; ALT_INIT.
CC	Matches 14; Mismatches 57; Indels 33; Gaps 8;	DR	DR: U66155; AAB07643.1; ALT_INIT.
CC	12 LLSLQLQGHGP-----DAR-----GVPVA-DGEFSSEQQVAKAGGTWLG 50	DR	DR: U7552.2; AAB18343.1; ALT_INIT.
CC	27 LIGHGRGPALPLRRPPRDLARLARLQAQRYLQGQDPAVDELRELSPWAIRPP-- 83	DR	DR: U7552.2; AAB08660.1; -.
CC	51 THRLPLKLRRLAISG--PQCLWPSLTSVLAELGGQASEEKVPIYACGSSCPGARTQHGLA 108	DR	DR: U49921; AAB5253.1; -.
CC	84 RRRAGPrrrrRrRrRGPcPGlRELEVRVSELGyTSDEtVLRyCAGACEAAIRI YDLG 142	DR	DR: DB8264; BAA1366.1; ALT_INIT.
CC	109 LARLQ----GGRAGGPPCRPRTYD-VAFIDDRHRWORLDQSLAAACGC 154	DR	DR: DB8352; BAB12221.1; -.
CC	143 LRLRQRRRrRrRrRERAHPCPRTAYEDFSEPDVHSRXYTQLELSARECAC 194	DR	DR: DB8352; BAB12221.1; JOINED.
CC	RESULTS 6	DR	DR: HSSP; Q07731; TAGQ.
CC	GDNF_MOUSE ID: P45540; P97919; STANDARD; PRT; 211 AA.	DR	DR: MGI:107430; Gdnf.
CC	DT 01-FEB-1996 (Rel. 33. Created)	DR	DR: IPK001839; TGFB.
CC	DT 01-FEB-1996 (Rel. 33. Last sequence update)	DR	DR: PS00250; TGF_Beta; 1.
CC	DT 16-OCT-2001 (Rel. 40. Last annotation update)	DR	DR: SHRT; SMD0204; TGF_beta; 1.
CC	DT 16-OCT-2001 (Rel. 40. Last annotation update)	DR	DR: PROSTE; PS00250; TGF_Beta; 1.
CC	GT: DISULFID 118 179	FT	FT: SIGNAL 1 19
CC	GT: DISULFID 145 208	FT	FT: BY SIMILARITY.
CC	GT: DISULFID 149 210	FT	FT: INTERCHAIN (BY SIMILARITY).
CC	GT: DISULFID 178 178	FT	FT: CARBOHYD 126 126
CC	GT: VARSPLIC 25 51	FT	FT: NLINKED (GCNCAC) (POTENTIAL).
CC	SQ SEQUENCE 211 AA: B5731C767A3A95B7 CRC64;	FT	FT: VARSPLIC 25 51
CC	GT: Query Match Best Local Similarity 21.2%; Score 177.5; DB 1; Length 211; Matches 47; Conservative 34.6%; Pred. No. 3./e-10; Indels 9; Gaps	FT	FT: SKRILLEAEDISLGHRRVPPALTSDS -> A (IN ISOFORM).
CC	GT: OC Mammalia; Etheria; Rodentia; Sciuromorphi; Murinae; Mus.	FT	FT: SEQUEL 211 AA: B5731C767A3A95B7 CRC64;
CC	GT: NCBI_TAXID=10990;	FT	FT: DISULFID 118 179
CC	GT: RN	FT	FT: DISULFID 145 208
CC	GT: RP	FT	FT: DISULFID 149 210
CC	GT: RC	FT	FT: CARBOHYD 126 126
CC	GT: STRAIN=C57BL/10J; TISSUE=Brain;	FT	FT: NLINKED (GCNCAC) (POTENTIAL).
CC	GT: RL Wang F., Too H.-P.;	FT	FT: VARSPLIC 25 51
CC	GT: RP Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.	FT	FT: SKRILLEAEDISLGHRRVPPALTSDS -> A (IN ISOFORM).
CC	GT: RN [2]	FT	FT: SEQUEL 211 AA: B5731C767A3A95B7 CRC64;
CC	GT: OC Tissue=Dorsal root ganglion;	FT	FT: DISULFID 118 179
CC	GT: RC STRAIN=ICR; TISSUE=Dorsal root ganglion;	FT	FT: DISULFID 145 208
CC	GT: OC Tissue=Dorsal root ganglion;	FT	FT: CARBOHYD 126 126
CC	GT: RC STRAIN=ICR; TISSUE=Dorsal root ganglion;	FT	FT: NLINKED (GCNCAC) (POTENTIAL).
CC	GT: OC Tissue=Dorsal root ganglion;	FT	FT: VARSPLIC 25 51
CC	GT: RC STRAIN=ICR; TISSUE=Dorsal root ganglion;	FT	FT: SKRILLEAEDISLGHRRVPPALTSDS -> A (IN ISOFORM).
CC	GT: OC Tissue=Dorsal root ganglion;	FT	FT: DISULFID 118 179
CC	GT: RC STRAIN=ICR; TISSUE=Dorsal root ganglion;	FT	FT: DISULFID 145 208
CC	GT: OC Tissue=Dorsal root ganglion;	FT	FT: CARBOHYD 126 126
CC	GT: RC STRAIN=ICR; TISSUE=Dorsal root ganglion;	FT	FT: NLINKED (GCNCAC) (POTENTIAL).
CC	GT: OC Tissue=Dorsal root ganglion;	FT	FT: VARSPLIC 25 51
CC	GT: RC STRAIN=ICR; TISSUE=Dorsal root ganglion;	FT	FT: SKRILLEAEDISLGHRRVPPALTSDS -> A (IN ISOFORM).
CC	GT: OC Tissue=Dorsal root ganglion;	FT	FT: DISULFID 118 179
CC	GT: RC STRAIN=ICR; TISSUE=Dorsal root ganglion;	FT	FT: DISULFID 145 208
CC	GT: OC Tissue=Dorsal root ganglion;	FT	FT: CARBOHYD 126 126
CC	GT: RC STRAIN=ICR; TISSUE=Dorsal root ganglion;	FT	FT: NLINKED (GCNCAC) (POTENTIAL).
CC	GT: OC Tissue=Dorsal root ganglion;	FT	FT: VARSPLIC 25 51
CC	GT: RC STRAIN=ICR; TISSUE=Dorsal root ganglion;	FT	FT: SKRILLEAEDISLGHRRVPPALTSDS -> A (IN ISOFORM).
CC	GT: OC Tissue=Dorsal root ganglion;	FT	FT: DISULFID 118 179
CC	GT: RC STRAIN=ICR; TISSUE=Dorsal root ganglion;	FT	FT: DISULFID 145 208
CC	GT: OC Tissue=Dorsal root ganglion;	FT	FT: CARBOHYD 126 126
CC	GT: RC STRAIN=ICR; TISSUE=Dorsal root ganglion;	FT	FT: NLINKED (GCNCAC) (POTENTIAL).
CC	GT: OC Tissue=Dorsal root ganglion;	FT	FT: VARSPLIC 25 51
CC	GT: RC STRAIN=ICR; TISSUE=Dorsal root ganglion;	FT	FT: SKRILLEAEDISLGHRRVPPALTSDS -> A (IN ISOFORM).
CC	GT: OC Tissue=Dorsal root ganglion;	FT	FT: DISULFID 118 179
CC	GT: RC STRAIN=ICR; TISSUE=Dorsal root ganglion;	FT	FT: DISULFID 145 208
CC	GT: OC Tissue=Dorsal root ganglion;	FT	FT: CARBOHYD 126 126
CC	GT: RC STRAIN=ICR; TISSUE=Dorsal root ganglion;	FT	FT: NLINKED (GCNCAC) (POTENTIAL).
CC	GT: OC Tissue=Dorsal root ganglion;	FT	FT: VARSPLIC 25 51
CC	GT: RC STRAIN=ICR; TISSUE=Dorsal root ganglion;	FT	FT: SKRILLEAEDISLGHRRVPPALTSDS -> A (IN ISOFORM).
CC	GT: OC Tissue=Dorsal root ganglion;	FT	FT: DISULFID 118 179
CC	GT: RC STRAIN=ICR; TISSUE=Dorsal root ganglion;	FT	FT: DISULFID 145 208
CC	GT: OC Tissue=Dorsal root ganglion;	FT	FT: CARBOHYD 126 126
CC	GT: RC STRAIN=ICR; TISSUE=Dorsal root ganglion;	FT	FT: NLINKED (GCNCAC) (POTENTIAL).
CC	GT: OC Tissue=Dorsal root ganglion;	FT	FT: VARSPLIC 25 51
CC	GT: RC STRAIN=ICR; TISSUE=Dorsal root ganglion;	FT	FT: SKRILLEAEDISLGHRRVPPALTSDS -> A (IN ISOFORM).
CC	GT: OC Tissue=Dorsal root ganglion;	FT	FT: DISULFID 118 179
CC	GT: RC STRAIN=ICR; TISSUE=Dorsal root ganglion;	FT	FT: DISULFID 145 208
CC	GT: OC Tissue=Dorsal root ganglion;	FT	FT: CARBOHYD 126 126
CC	GT: RC STRAIN=ICR; TISSUE=Dorsal root ganglion;	FT	FT: NLINKED (GCNCAC) (POTENTIAL).
CC	GT: OC Tissue=Dorsal root ganglion;	FT	FT: VARSPLIC 25 51
CC	GT: RC STRAIN=ICR; TISSUE=Dorsal root ganglion;	FT	FT: SKRILLEAEDISLGHRRVPPALTSDS -> A (IN ISOFORM).
CC	GT: OC Tissue=Dorsal root ganglion;	FT	FT: DISULFID 118 179
CC	GT: RC STRAIN=ICR; TISSUE=Dorsal root ganglion;	FT	FT: DISULFID 145 208
CC	GT: OC Tissue=Dorsal root ganglion;	FT	FT: CARBOHYD 126 126
CC	GT: RC STRAIN=ICR; TISSUE=Dorsal root ganglion;	FT	FT: NLINKED (GCNCAC) (POTENTIAL).
CC	GT: OC Tissue=Dorsal root ganglion;	FT	FT: VARSPLIC 25 51
CC	GT: RC STRAIN=ICR; TISSUE=Dorsal root ganglion;	FT	FT: SKRILLEAEDISLGHRRVPPALTSDS -> A (IN ISOFORM).
CC	GT: OC Tissue=Dorsal root ganglion;	FT	FT: DISULFID 118 179
CC	GT: RC STRAIN=ICR; TISSUE=Dorsal root ganglion;	FT	FT: DISULFID 145 208
CC	GT: OC Tissue=Dorsal root ganglion;	FT	FT: CARBOHYD 126 126
CC	GT: RC STRAIN=ICR; TISSUE=Dorsal root ganglion;	FT	FT: NLINKED (GCNCAC) (POTENTIAL).
CC	GT: OC Tissue=Dorsal root ganglion;	FT	FT: VARSPLIC 25 51
CC	GT: RC STRAIN=ICR; TISSUE=Dorsal root ganglion;	FT	FT: SKRILLEAEDISLGHRRVPPALTSDS -> A (IN ISOFORM).
CC	GT: OC Tissue=Dorsal root ganglion;	FT	FT: DISULFID 118 179
CC	GT: RC STRAIN=ICR; TISSUE=Dorsal root ganglion;	FT	FT: DISULFID 145 208
CC	GT: OC Tissue=Dorsal root ganglion;	FT	FT: CARBOHYD 126 126
CC	GT: RC STRAIN=ICR; TISSUE=Dorsal root ganglion;	FT	FT: NLINKED (GCNCAC) (POTENTIAL).
CC	GT: OC Tissue=Dorsal root ganglion;	FT	FT: VARSPLIC 25 51
CC	GT: RC STRAIN=ICR; TISSUE=Dorsal root ganglion;	FT	FT: SKRILLEAEDISLGHRRVPPALTSDS -> A (IN ISOFORM).
CC	GT: OC Tissue=Dorsal root ganglion;	FT	FT: DISULFID 118 179
CC	GT: RC STRAIN=ICR; TISSUE=Dorsal root ganglion;	FT	FT: DISULFID 145 208
CC	GT: OC Tissue=Dorsal root ganglion;	FT	FT: CARBOHYD 126 126
CC	GT: RC STRAIN=ICR; TISSUE=Dorsal root ganglion;	FT	FT: NLINKED (GCNCAC) (POTENTIAL).
CC	GT: OC Tissue=Dorsal root ganglion;	FT	FT: VARSPLIC 25 51
CC	GT: RC STRAIN=ICR; TISSUE=Dorsal root ganglion;	FT	FT: SKRILLEAEDISLGHRRVPPALTSDS -> A (IN ISOFORM).
CC	GT: OC Tissue=Dorsal root ganglion;	FT	FT: DISULFID 118 179
CC	GT: RC STRAIN=ICR; TISSUE=Dorsal root ganglion;	FT	FT: DISULFID 145 208
CC	GT: OC Tissue=Dorsal root ganglion;	FT	FT: CARBOHYD 126 126
CC	GT: RC STRAIN=ICR; TISSUE=Dorsal root ganglion;	FT	FT: NLINKED (GCNCAC) (POTENTIAL).
CC	GT: OC Tissue=Dorsal root ganglion;	FT	FT: VARSPLIC 25 51
CC	GT: RC STRAIN=ICR; TISSUE=Dorsal root ganglion;	FT	FT: SKRILLEAEDISLGHRRVPPALTSDS -> A (IN ISOFORM).
CC	GT: OC Tissue=Dorsal root ganglion;	FT	FT: DISULFID 118 179
CC	GT: RC STRAIN=ICR; TISSUE=Dorsal root ganglion;	FT	FT: DISULFID 145 208
CC	GT: OC Tissue=Dorsal root ganglion;	FT	FT: CARBOHYD 126 126
CC	GT: RC STRAIN=ICR; TISSUE=Dorsal root ganglion;	FT	FT: NLINKED (GCNCAC) (POTENTIAL).
CC	GT: OC Tissue=Dorsal root ganglion;	FT	FT: VARSPLIC 25 51
CC	GT: RC STRAIN=ICR; TISSUE=Dorsal root ganglion;	FT	FT: SKRILLEAEDISLGHRRVPPALTSDS -> A (IN ISOFORM).
CC	GT: OC Tissue=Dorsal root ganglion;	FT	FT: DISULFID 118 179
CC	GT: RC STRAIN=ICR; TISSUE=Dorsal root ganglion;	FT	FT: DISULFID 145 208
CC	GT: OC Tissue=Dorsal root ganglion;	FT	FT: CARBOHYD 126 126
CC	GT: RC STRAIN=ICR; TISSUE=Dorsal root ganglion;	FT	FT: NLINKED (GCNCAC) (POTENTIAL).
CC	GT: OC Tissue=Dorsal root ganglion;	FT	FT: VARSPLIC 25 51
CC	GT: RC STRAIN=ICR; TISSUE=Dorsal root ganglion;	FT	FT: SKRILLEAEDISLGHRRVPPALTSDS -> A (IN ISOFORM).
CC	GT: OC Tissue=Dorsal root ganglion;	FT	FT: DISULFID 118 179
CC	GT: RC STRAIN=ICR; TISSUE=Dorsal root ganglion;	FT	FT: DISULFID 145 208
CC	GT: OC Tissue=Dorsal root ganglion;	FT	FT: CARBOHYD 126 126
CC	GT: RC STRAIN=ICR; TISSUE=Dorsal root ganglion;	FT	FT: NLINKED (GCNCAC) (POTENTIAL).
CC	GT: OC Tissue=Dorsal root ganglion;	FT	FT: VARSPLIC 25 51
CC	GT: RC STRAIN=ICR; TISSUE=Dorsal root ganglion;	FT	FT: SKRILLEAEDISLGHRRVPPALTSDS -> A (IN ISOFORM).
CC	GT: OC Tissue=Dorsal root ganglion;	FT	FT: DISULFID 118 179
CC	GT: RC STRAIN=ICR; TISSUE=Dorsal root ganglion;	FT	FT: DISULFID 145 208
CC	GT: OC Tissue=Dorsal root ganglion;	FT	FT: CARBOHYD 126 126
CC	GT: RC STRAIN=ICR; TISSUE=Dorsal root ganglion;	FT	FT: NLINKED (GCNCAC) (POTENTIAL).
CC	GT: OC Tissue=Dorsal root ganglion;	FT	FT: VARSPLIC 25 51
CC	GT: RC STRAIN=ICR; TISSUE=Dorsal root ganglion;	FT	FT: SKRILLEAEDISLGHRRVPPALTSDS -> A (IN ISOFORM).
CC	GT: OC Tissue=Dorsal root ganglion;	FT	FT: DISULFID 118 179
CC	GT: RC STRAIN=ICR; TISSUE=Dorsal root ganglion;	FT	FT: DISULFID 145 208
CC	GT: OC Tissue=Dorsal root ganglion;	FT	FT: CARBOHYD 126 126
CC	GT: RC STRAIN=ICR; TISSUE=Dorsal root ganglion;	FT	FT: NLINKED (GCNCAC) (POTENTIAL).
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CC	GT: OC Tissue=Dorsal root ganglion;	FT	FT: DISULFID 118 179
CC	GT: RC STRAIN=ICR; TISSUE=Dorsal root ganglion;	FT	FT: DISULFID 145 208
CC	GT: OC Tissue=Dorsal root ganglion;	FT	FT: CARBOHYD 126 126
CC	GT: RC STRAIN=ICR; TISSUE=Dorsal root ganglion;	FT	FT: NLINKED (GCNCAC) (POTENTIAL).
CC	GT: OC Tissue=Dorsal root ganglion;	FT	FT: VARSPLIC 25 51
CC	GT: RC STRAIN=ICR; TISSUE=Dorsal root ganglion;	FT	FT: SKRILLEAEDISLGHRRVPPALTSDS -> A (IN ISOFORM).
CC	GT: OC Tissue=Dorsal root ganglion;	FT	FT: DISULFID 118 179
CC	GT: RC STRAIN=ICR; TISSUE=Dorsal root ganglion;	FT	FT: DISULFID 145 208
CC	GT: OC Tissue=Dorsal root ganglion;	FT	FT: CARBOHYD 126 126
CC	GT: RC STRAIN=ICR; TISSUE=Dorsal root ganglion;	FT	FT: NLINKED (GCNCAC) (POTENTIAL).
CC	GT: OC Tissue=Dorsal root ganglion;	FT	FT: VARSPLIC 25 51
CC	GT: RC STRAIN=ICR; TISSUE=Dorsal root ganglion;	FT	FT: SKRILLEAEDISLGHRRVPPALTSDS -> A (IN ISOFORM).
CC	GT: OC Tissue=Dorsal root ganglion;	FT	FT: DISULFID 118 179
CC	GT: RC STRAIN=ICR; TISSUE=Dorsal root ganglion;	FT	FT: DISULFID 145 208
CC	GT: OC Tissue=Dorsal root ganglion;	FT	FT: CARBOHYD 126 126
CC	GT: RC STRAIN=ICR; TISSUE=Dorsal root ganglion;	FT	FT: NLINKED (GCNCAC) (POTENTIAL).
CC	GT: OC Tissue=Dorsal root ganglion;	FT	FT: VARSPLIC 25 51
CC	GT: RC STRAIN=ICR; TISSUE=Dorsal root ganglion;	FT	FT: SKRILLEAEDISLGHRRVPPALTSDS -> A (IN ISOFORM).
CC	GT: OC Tissue=Dorsal root ganglion;	FT	FT: DISULFID 118 179
CC	GT: RC STRAIN=ICR; TISSUE=Dorsal root ganglion;	FT	FT: DISULFID 145 208
CC	GT: OC Tissue=Dorsal root ganglion;	FT	FT: CARBOHYD 126 126
CC	GT: RC STRAIN=ICR; TISSUE=Dorsal root ganglion;	FT	FT: NLINKED (GCNCAC) (POTENTIAL).
CC	GT: OC Tissue=Dorsal root ganglion;	FT	FT: VARSPLIC 25 51
CC	GT: RC STRAIN=ICR; TISSUE=Dorsal root ganglion;	FT	FT: SKRILLEAEDISLGHRRVPPALTSDS -> A (IN ISOFORM).
CC	GT: OC Tissue=Dorsal root ganglion;	FT	FT: DISULFID 118 179
CC	GT: RC STRAIN=ICR; TISSUE=Dorsal root ganglion;	FT	FT: DISULFID 145 208
CC	GT: OC Tissue=Dorsal root ganglion;	FT	FT: CARBOHYD 126 126
CC	GT: RC STRAIN=ICR; TISSUE=Dorsal root ganglion;	FT	FT: NLINKED (GCNCAC) (POTENTIAL).
CC	GT: OC Tissue=Dorsal root ganglion;	FT	FT: VARSPLIC 25 51
CC	GT: RC STRAIN=ICR; TISSUE=Dorsal root ganglion;	FT	FT: SKRILLEAEDISLGHRRVPPALTSDS -> A (IN ISOFORM).
CC	GT: OC Tissue=Dorsal root ganglion;	FT	FT: DISULFID 118 179
CC	GT: RC STRAIN=ICR; TISSUE=Dorsal root ganglion;	FT	FT: DISULFID 145 208
CC	GT: OC Tissue=Dorsal root ganglion;	FT	FT: CARBOHYD 126 126
CC	GT: RC STRAIN=ICR; TISSUE=Dorsal root ganglion;	FT	FT: NLINKED (GCNCAC) (POTENTIAL).
CC	GT: OC Tissue=Dorsal root ganglion;	FT	FT: VARSPLIC 25 51
CC	GT: RC STRAIN=ICR; TISSUE=Dorsal root ganglion;	FT	FT: SKRILLEAEDISLGHRRVPPALTSDS -> A (IN ISOFORM).
CC	GT: OC Tissue=Dorsal root ganglion;	FT	FT: DISULFID 118 179
CC	GT: RC STRAIN=ICR; TISSUE=Dorsal root ganglion;	FT	FT: DISULFID 145 208
CC	GT: OC Tissue=Dorsal root ganglion;	FT	FT: CARBOHYD 126 126
CC	GT: RC STRAIN=ICR; TISSUE=Dorsal root ganglion;	FT	FT: NLINKED (GCNCAC) (POTENTIAL).
CC	GT: OC Tissue=Dorsal root ganglion;	FT	FT: VARSPLIC 25 51
CC	GT: RC STRAIN=ICR; TISSUE=Dorsal root ganglion;	FT	FT: SKRILLEAEDISLGHRRVPPALTSDS -> A (IN ISOFORM).
CC	GT: OC Tissue=Dorsal root ganglion;	FT	FT: DISULFID 118 179
CC	GT: RC STRAIN=ICR; TISSUE=Dorsal root ganglion;	FT	FT: DISULFID 145 208
CC	GT: OC Tissue=Dorsal root ganglion;	FT</	

Result No.	Score	Query	Match	Length	DB	ID	Description
1	244	SPTREMBL_21:*	1:	sp_archaea:*			096030 homo sapien
2	244	SPTREMBL_21:*	2:	sp_bacteria:*			095441 homo sapien
3	839	Perfect score: 839	3:	sp_fungi:*			092102 mus musculus
Sequence: 1 MAVGKFLGSLLSLIGQ... .... DRHRWORLDQLSAAACGGGG 156			4:	sp_human:*			099290 rattus norvegicus
Scoring table: BLOSUM62			5:	sp_invertebrate:*			097685 macaca mulatta
Title: Gapext 10.0 , Gapext 0.5			6:	sp_mammal:*			096322 homo sapiens
Target: 671580 seqs, 2064715 residues			7:	sp_mhc:*			096153 rhesus macaque
Total number of hits satisfying chosen parameters: 671580			8:	sp_organelle:*			098152 rhesus macaque
Minimum DB seq length: 0			9:	sp_phage:*			098153 rhesus macaque
Maximum DB seq length: 2000000000			10:	sp_plant:*			098154 rhesus macaque
Post-processing: Maximum Match 0%			11:	sp_rhodent:*			098155 rhesus macaque
Listing first 45 summaries			12:	sp_virus:*			098156 rhesus macaque
Database : SPTREMBL_21:*			13:	sp_vertebrate:*			098157 rhesus macaque
			14:	sp_unclassified:*			098158 rhesus macaque
			15:	sp_rvirus:*			098159 rhesus macaque
			16:	sp_bacterioplasm:*			098160 rhesus macaque
			17:	sp_archeap:*			098161 rhesus macaque
							098162 rhesus macaque
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